

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 219

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: U.S.A.
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.
(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TACAGACTTC	ACAGAGAATG	CAGTTGTCTT	GACTTCAGGT	CTGTCTGTTC	60
TGTTGGCAAG	TAAATGCAGT	ACTGTTCTGA	TCCCGCTGCT	ATTAGAATGC	ATTGTGAAAC	120
GACTGGAGTA	TGATTAAAAG	TTGTGTTCCC	CAATGCTTGG	AGTAGTGATT	GTTGAAGGAA	180
AAAATCCAGC	TGAGTGATAA	AGGCTGAGTG	TTGAGGAAAT	TTCTGCAGTT	TTAAGCAGTC	240
GTATTTGTGA	TTGAAGCTGA	GTACATTTTG	CTGGTGTATT	TTTAGGTAAA	ATGCTTTTTG	300
TTCATTTCTG	GTGGTGGGAG	GGGACTGAAG	CCTTTAGTCT	TTCCAGATG	CAACCTTAAA	360
ATCAGTGACA	AGAAACATTC	CAAACAAGCA	ACAGTCTTCA	AGAAATTAAA	CTGGCAAGTG	420
GAAATGTTTA	AACAGTTCAG	TGATCTTTAG	TGCATTGTTT	ATGTGTGGGT	TTCTCTCTCC	480
CCTCCCTTGG	TCTTAATTCT	TACATGCAGG	AACACTCAGC	AGACACACGT	ATGCGAAGGG	540
CCAGAGAAGC	CAGACCCAGT	AAGAAAAAAT	AGCCTATTTA	CTTTAAATAA	ACCAAACATT	600
CCATTTTAAA	TGTGGGGATT	GGGAACCACT	AGTTCTTTCA	GATGGTATTC	TTCAGACTAT	660
AGAAGGAGCT	TCCAGTTGAA	TTCACCAGTG	GACAAAATGA	GGAAAACAGG	TGAACAAGCT	720
TTTTCTGTAT	TTACATACAA	AGTCAGATCA	GTTATGGGAC	AATAGTATTG	AATAGATTTT	780
AGCTTTATGC	TGGAGTAACT	GGCATGTGAG	CAAACGTGTG	TGGCGTGGGG	GTGGAGGGGT	840
GAGGTGGGCG	CTAAGCTTTT	TTTAAGATTT	TTCAGGTACC	CTTCACTAAA	GGCACCGAAG	900
GCTTAAAGTA	GGACAACCAT	GGAGCTTCCT	GTGGCAGGAG	AGACAACAAA	GCGCTATTAT	960
CCTAAGGTCA	AGAGAAGTGT	CAGCCTCACC	TGATTTTTAT	TAGTAATGAG	GACTTGCCTC	1020
AACTCCCTCT	TTCTGGAGTG	AAGCATCCGA	AGGAATGCTT	GAAGTACCCC	TGGGCTTCTC	1080
TTAACATTTA	AGCAAGCTGT	TTTTATAGCA	GCTCTTAATA	ATAAAGCCCA	AATCTCAAGC	1140
GGTGCTTGAA	GGGGAGGGAA	AGGGGGAAAG	CGGGCAACCA	CTTTTCCCTA	GCTTTTCCAG	1200
AAGCCTGTTA	AAAGCAAGGT	CTCCCCACAA	GCAACTTCTC	TGCCACATCG	CCACCCCGTG	1260
CCTTTTGATC	TAGCACAGAC	CCTTCACCCC	TCACCTCGAT	GCAGCCAGTA	GCTTGGATCC	1320
TTGTGGGCAT	GATCCATAAT	CGGTTTCAAG	GTAACGATGG	TGTCGAGKTC	TTTGGTGGGT	1380
TGAACTATGT	TAGAAAAGGC	CATTAATTTG	CCTGCAAATT	GTTAACAGAA	GGGTATTAAA	1440
ACCACAGCTA	AGTAGCTCTA	TTATAATACT	TATCCAGTGA	CTAAAACCAA	CTTAAACCAG	1500
TAAGTGGAGA	AATAACATGT	TCAAGAACTG	TAATGCTGGG	TGGGAACATG	TAAGTTGTAG	1560
ACTGGAGAAG	ATAGGCATTT	GAGTGGCTGA	GAGGGCTTTT	GGGTGGGAAT	GCAAAAATTC	1620

TCTGCTAAGA CTTTTTCAGG TGAACATAAC AGACTTGGCC AAGCTAGCAT CTTAGCGGAA 1680
 GCTGATCTCC AATGCTCTTC AGTAGGGTCA TGAAGGTTTT TCTTTTCCTG AGAAAACAAC 1740
 ACGTATTGTT TTCTCAGGTT TTGCTTTTTG GCCTTTTTCT AGCTTAAAAA AAAAAAAAAA 1800

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Trp Val Ser Leu Ser Pro Pro Leu Val Leu Ile Leu Thr Cys Arg
 1 5 10 15
 Asn Thr Gln Gln Thr His Val Cys Glu Gly Pro Glu Lys Pro Asp Pro
 20 25 30
 Val Arg Lys Asn Ser Leu Phe Thr Leu Asn Lys Pro Asn Ile Pro Phe
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1063 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAAGTTCCAT CTCTAGAACT GATTTTTATC CGTTCTGTTT TTCAGGTCTT ATCTGTGTTA 60
 GTTGTGTGTT ACTATCAGGA GGCCCCCTTT GGACCCAGTG GATACAGATT ACGACTCTTC 120
 TTTTATGGTG TATGCAATGT CATTTCTATC ACTTGTGCTT ATACATCATT TTCAATAGTT 180
 CCTCCCAGCA ATGGGACCAC TATGTGGAGA GCCACAATA CAGTCTTCAG TGCCATTTTG 240
 GCTTTTTTAC TCGTAGATGA GAAAATGGCT TATGTTGACA TGGCTACAGT TGTTTGCAGC 300
 ATCTTAGGTG TTTGTCTTGT CATGATCCCA AACATTGTTG ATGAAGACAA TTCTTTGTTA 360

AATGCCTGGA AAGAAGCCTT TGGGTACACC ATGACTGTGA TGGCTGGACT GACCACTGCT 420
 CTCTCAATGA TAGTATACAG ATCCATCAAG GAGAAGATCA GCATGTGGAC TGCCTGTTT 480
 ACTTTTGGTT GGACTGGGAC AATTTGGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC 540
 ATCATCCCAT TAGATGGAGA AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT 600
 GCAGCATTCT TAGGAGTTTA TTATGCCTTG GACAAATTCC ATCCAGCTTT GGTAGCACA 660
 GTACAACATT TGGAGATTGT GGTAGCTATG GTCTTGCAGC TTCTCGTGCT GCACATATTT 720
 CCTAGCATCT ATGATGTTTT TGGAGGGGTA ATCATTATGA TTAGTGTTTT TGTCTTGCT 780
 GGCTATAAAC TTTACTGGAG GAATTTAAGA AGGCAGGACT ACCAGGAAAT ATTAGACTCT 840
 CCCATTAAAT GAATACCTGA TTATTATTGT CTCATTAATG TTCAGTTATT AATATGTATA 900
 CTGCCATTTT AATGTTTACC TATGAATGTC TTTTGTGTTA TATAACTGAC AGAGTGCTAT 960
 AAAATATATA ATATATACAA ATGCAGAAAA TTTATTCTAG TCTAATATAT TCAAATACAA 1020
 ATATTAAATA TATGAAATAC GTTAAAAAAA AAAAAAAAAA AAA 1063

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Trp	Arg	Ala	Thr	Thr	Thr	Val	Phe	Ser	Ala	Ile	Leu	Ala	Phe	Leu
1				5					10				15		
Leu	Val	Asp	Glu	Lys	Met	Ala	Tyr	Val	Asp	Met	Ala	Thr	Val	Val	Cys
		20						25				30			
Ser	Ile	Leu	Gly	Val	Cys	Leu	Val	Met	Ile	Pro	Asn	Ile	Val	Asp	Glu
		35					40					45			
Asp	Asn	Ser	Leu	Leu	Asn	Ala	Trp	Lys	Glu	Ala	Phe	Gly	Tyr	Thr	Met
	50					55					60				
Thr	Val	Met	Ala	Gly	Leu	Thr	Thr	Ala	Leu	Ser	Met	Ile	Val	Tyr	Arg
65					70					75				80	
Ser	Ile	Lys	Glu	Lys	Ile	Ser	Met	Trp	Thr	Ala	Leu	Phe	Thr	Phe	Gly
			85					90					95		
Trp	Thr	Gly	Thr	Ile	Trp	Gly	Ile	Ser	Thr	Met	Phe	Ile	Leu	Gln	Glu

100	105	110
Pro Ile Ile Pro Leu Asp Gly Glu Thr Trp Ser Tyr Leu Ile Ala Ile		
115	120	125
Cys Val Cys Ser Thr Ala Ala Phe Leu Gly Val Tyr Tyr Ala Leu Asp		
130	135	140
Lys Phe His Pro Ala Leu Val Ser Thr Val Gln His Leu Glu Ile Val		
145	150	155
Val Ala Met Val Leu Gln Leu Leu Val Leu His Ile Phe Pro Ser Ile		
	165	170
Tyr Asp Val Phe Gly Gly Val Ile Ile Met Ile Ser Val Phe Val Leu		
	180	185
Ala Gly Tyr Lys Leu Tyr Trp Arg Asn Leu Arg Arg Gln Asp Tyr Gln		
	195	200
Glu Ile Leu Asp Ser Pro Ile Lys		
210	215	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGCCAAAGA GGCCTAGCCG GGAGCGGGCG AGGCGGCGGC GGCAGCAGCG ATGGCAGGAA	60
TAGAGTTGGA GCGGTGCCAG CAGCAGGCGA ACGAGGTGAC GGAAATTATG CGTAACAAC	120
TCGGCAAGGT CCTGGAGCGT GGTGTGAAGC TGGCCGAAC	180
GCAGCAGCGT TCAGACCAAC	
TCCTGGATAT GAGCTCAACC TTCAACAAGA CTACACAGAA CCTGGCCCAG AAGAAGTGCT	240
GGGAGAACAT CCGTTACCGG ATCTGCGTGG GGCTGGTGGT GGTTGGTGTC CTGCTCATCA	300
TCCTGATTGT GCTGCTGGTC GTCTTTCTCC CTCAGAGCAG TGACAGCAGT AGTGCC	356

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ala Gly Ile Glu Leu Glu Arg Cys Gln Gln Gln Ala Asn Glu Val
 1             5             10             15

Thr Glu Ile Met Arg Asn Asn Phe Gly Lys Val Leu Glu Arg Gly Val
 20             25             30

Lys Leu Ala Glu Leu Gln Gln Arg Ser Asp Gln Leu Leu Asp Met Ser
 35             40             45

Ser Thr Phe Asn Lys Thr Thr Gln Asn Leu Ala Gln Lys Lys Cys Trp
 50             55             60

Glu Asn Ile Arg Tyr Arg Ile Cys Val Gly Leu Val Val Val Gly Val
 65             70             75             80

Leu Leu Ile Ile Leu Ile Val Leu Leu Val Val Phe Leu Pro Gln Ser
 85             90             95

Ser Asp Ser Ser Ser Ala
 100
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 92
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGCCTCAAC TTTGGCGTCG TGAGATTCTT GTGAGGCGTC TGCCTGGAAG CCGGCAGCAA 60
TTTTGCTTCT TTAAAGAGAA AAAGAAGGCT AGGGACTCAG ATTCTTGGAT TCTGAGATCC 120
AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCCTCGT ATCCAGCATT 180
TGCTGATCCT CCTGGTCCTA GGAGCCTCCC TCCTGACCTC GGGCCTAGAG CTGTATTGTC 240
AAAAGGGTCT GTCCATGACT GTGGAAGCAG ATCCAGCCAA TATGTTTAAC TGGACCACAG 300
AGGAAGTGGA GACTTGTGAC AAAGGGGCAC TTTGCCAGGA AACCATACTA ATAATTAAAG 360
CAGGGACTGA GACAGCCATT TTGGCCACGA AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA 420
TAACAATTGT CCAGCACTCT TCACCTCCCG GCCTGATCGT GACCTCCTAC AGTAACTACT 480
GTGAGGATTC CTTCTGTAAT GACAAAGACA GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA 540
CCACAGCTTC CACTGTGTCA ACAACCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT 600
GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA ATGGTACAAC TCGATGCTAT CAAGGAAAAC 660
TTGAGATCAC TGGAGGTGGC ATTGAGTCGT CTGTGGAGGT CAAAGGCTGT ACAGCCATGA 720
TTGGCTGCAG GCTGATGTCT GGAATCTTAG CAGTAGGACC CATGTTTGTG AGGGAAGCGT 780
GCCCACATCA GCTGCTCACT CAACCTCGAA AGACTGAAAA TGGGGCCACC TGTCTTCCCA 840
TTCCTGTTTG GGGGTACAG CTA CTGCTGC CATTGCTGCT GCCATCATT ATTCACTTTT 900
CCTAAGAAGG CACTTCTGGG CCTGGGTCTG AGGACATCTT TTTTGA CTGG GAGCCTTCTT 960
ACTGTTGAGG TTCAACAAGC TGAGGAGTAG ATGGGAATTT GAGGGAGAAT ACAGAGATAC 1020
TATGAACGTA TTTGACATTT TTAATACAAT TTCTGCTATA ATTTTGTAT GCAGTAGGCG 1080
TTACTAATAA ACATTTCTGC TGTGAAAAAA AAAAAAAAAA AAAAAAAAAA A 1131

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Thr Pro Arg Ile Gln His Leu Leu Ile Leu Leu Val Leu Gly
1 5 10 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCCGGGCC	GGCTGCGGAG	CGACTCCCCG	CCGCCAAGTG	GGCGGCGTGG	CTGTCTGGGAA	60
AGAAGGGCTG	GGGCCTGCCG	TTCTTCCTCC	CGAGTATCCC	CTCCAGCTGG	ACGACCCAC	120
GCTGCAGCAC	GGGCTTCCGG	CTTCTCTCCT	CAGTGGCCAA	TTCGAGGGCA	CAGCGGGCTC	180
CGGAGGCGCG	GCGGCAAGCC	TATCCCGCCT	CCCAACCACA	GCCTCCAGCA	CCCAGAGAA	240
CGGCCGCCCA	CAGCACACGT	TCTCCGACA	GGAGGGCGAA	GGCCCAAGAC	CTGGAGAGAT	300
GGTCAGCTCT	CAAAAAAGGC	ACAAACAATT	GAAGGATGGA	TACCATGGCA	TATGTTAAAA	360
GCGTGTTGAA	AGGAAAATAA	GAAAGCCAGG	AATCTCAGGA	TGAATCAGTC	TAGATCGAGA	420
TCAGATGGTG	GCAGTGAAGA	AACCTTACCT	CAAGACCATA	ATCATCATGA	AAATGAGAGA	480
AGATGGCAGC	AAGAGCGTCT	CCACAGAGAA	GAGGCCTATT	ATCAGTTTAT	TAATGAACTC	540
AATGATGAAG	ATTATCGGCT	TATGAGAGAC	CATAATCTTT	TAGGCACCCC	TGGAGAAATA	600
ACATCAGAAG	AACTGCAACA	GCGGTTAGAT	GGCGTCAAGG	AACAAC TAGC	ATCTCAGCCT	660
GACTTGAGAG	ATGGAACGAA	TTACAGAGAC	TCAGAAGTCC	CTAGAGAAAG	TTCACATGAA	720
GATTCTCTTC	TAGAATGGTT	GAACACCTTT	CGGCGCACAG	GAAATGCAAC	TCGAAGTGGA	780
CAAAATGGGA	ACCAAAC TTG	GAGAGCTGTG	AGTCGAACAA	ACCCGAACAA	TGGAGAGTTT	840
CGGTTTAGTT	TGGAAATCCA	CGTAAATCAT	GAAAATAGAG	GATTTGAAAT	TCATGGAGAA	900
GATTATACAG	ACATTCCACT	TTCAGATAGT	AACAGAGATC	ATACTGCAAA	TAGGCAACAA	960
AGGTCAACTA	GTCCTGTGGC	TAGGCGAACA	AGAAGCCAAA	CCTCAGTGAA	TTTCAATGGT	1020
AGTAGTTCCA	ACATTCCAAG	GA CTAGGCTT	GCTTCAAGGG	GGCAAAATCC	AGCTGAAGGA	1080
TCTTTCTCAA	CATTGGGAAG	GTTAAGAAAT	GGAATTGGGG	GAGCAGCTGG	CATTCTCTCGA	1140
GCTAACGCTT	CACGCACTAA	TTTCAGTAGT	CACACAAACC	AATCAGGTGG	TAGTGAATCTC	1200
AGGCAAAGGG	AGGGGCAACG	GTTTGGAGCA	GCACATGTTT	GGGAAAATGG	GGCTAGAAGT	1260
AATGTTACAG	TGAGGAATAC	AAACCAAAGA	TTAGAGCCAA	TAAGATTACG	ATCTACTTCC	1320
AATAGTCGAA	GCCGTTCAAC	AATTCAGAGA	CAGAGTGGCA	CTGTTTATCA	TAATTCCCAA	1380
AGGGAAAGTA	GACCAGTACA	GCAAACCACT	AGAAGATCTG	TTAGGAGGAG	AGGTAGAACT	1440
CGAGTCTTTT	TAGAGCAAGA	TAGAGAACGA	GAACGCAGAG	GTACTGCATA	TACCCCATTC	1500
TCTAATTCAA	GGCTTG TGTC	AAGAATAACA	GTAGAAGAAG	GAGAAGAATC	CAGCAGATCC	1560
TCAACTGCTG	TACGACGACA	TCCAACAATC	ACACTGGACC	TTCAAGTGAG	AAGGATCCGT	1620

CCTGGAGAAA	ATAGAGATCG	GGATAGTATT	GCAAATAGAA	CTCGATCCAG	AGTAGGGCTA	1680
GCAGAAAATA	CAGTCACTAT	TGAAAGCAAT	AGTGGGGGCT	TTCGCCGAAC	CATTTCTCGT	1740
TTAGAGCGGT	CAGGTATTCG	AACCTATGTT	AGTACCATAA	CAGTTCCCCT	TCGTAGGATT	1800
TCTGAGAATG	AGCTTGTTGA	GCCATCATCA	GTGGCTCTTC	GGTCAATTTT	AAGGCAGATC	1860
ATGACTGGGT	TTGGAGAACT	GAGTTCTCTA	ATGGAGGCCG	ATTCTGAGTC	AGAACTTCAA	1920
AGAAATGGCC	AGCATTTACC	AGACATGCAC	TCAGAACTGA	GTAACCTAGG	TACAGATAAC	1980
AACAGGAGCC	AGCACAGGGA	AGGTTCCCTCT	CAAGACAGGC	AGGCCCAAGG	AGACAGCACT	2040
GAAATGCATG	GTGAAAACGA	GACCACCCAG	CCTCATACTC	GAAACAGTGA	CAGTAGGGGT	2100
GGCAGGCAGT	TGCGAAATCC	AAACAATTTA	GTTGAAACTG	GAACACTACC	CATTCTTCGC	2160
CTTGCTCACT	TTTTTTTACT	AAATGAAAGT	GATGATGATG	ATCGAATACG	TGGTTTAACC	2220
AAAGAGCAGA	TTGACAATCT	TTCCACCAGG	CACTATGAGC	ATAACAGTAT	TGATAGTGAA	2280
CTAGGTAAAA	TCTGTAGTGT	TTGTATTAGT	GACTATGTAA	CTGGAAACAA	GCTCAGGCAA	2340
TTACCTTGCA	TGCATGAATT	TCACATTCAT	TGTATTGACC	GATGGCTCTC	AGAGAATTGC	2400
ACTTGTC CGA	TCTGTCGGCA	GCCTGTTTTA	GGGTCTAACA	TAGCAAACAA	TGGGTAAGGT	2460
GATGGGATCT	ACTCAAATAC	TGTTTTTTAG	TAGAACTGAA	TGTTCAAGCA	TTGTTTTGCT	2520
GAGTTATTTG	TGATTAGCTA	ACCAGGATGA	AAAATAACAG	ATTATATATA	GTTTGAACTA	2580
TTTTTCGTGT	GCTTTTTTAA	ACTTGTTAAA	AAGAAATTTA	TATAAAATTT	AAAATACAAA	2640
TGTAAATTA	TCCAGAAATA	CAGAATAGTT	AATATTGCTA	GAACCAAATA	ACCTCTAAAA	2700
TGTTTTTATT	TTGGTAATTT	TGTCATGCTA	AGCACTTTTG	TATCTGCACA	ATTCAGTAGG	2760
TTAAGAATCA	ATCTTCTTTT	TCTTAATAGT	ACAGCAGACT	TTAGCTTCAA	GTTTCATAGG	2820
CTTAGTACTT	ATATCTAGAC	ATTTGTGTCT	AAATAAGCTT	TTCATTAACT	TTTTATTTTA	2880
AGGACAGTAT	CTTTTCATGA	AAGAGTATTT	GGCTGAATGT	TTGCTATATA	TATGTTACTT	2940
GAAATGTTAA	ATTTAATATG	CAGCATACCA	TAGGTGTATA	TATAGGTATA	TAATTTTAAG	3000
GTTAAAATAT	TCAGTCTAAC	AAGTTTG GTT	CTTATTTAAG	CTTTTGGGCT	AATACTGCAT	3060
ATGGCACAAAT	GTTTAATATT	GGCAAGTTCA	TCTCAGAGAA	AGGGGATTCA	GATATAATTT	3120
TAAAGTAGAG	ATAATTTACT	GAAGCGTCTC	TGACAATCTA	ACTTATTAGA	CAGCAAGCAA	3180
TATATAATAC	TGAAAAAGTA	TTCAGAAAATG	GAAAATTTAC	ATCATATAGG	TTATTTAACT	3240
TGTGTT CAGC	CTTTTTGTAA	CTTTTTTGAA	AGTGCAAACA	ATTCTTTGGA	TTATTAAATA	3300

AGGTATACAG TATGCATGGT TTCTCAAATT TAGCTTTAAA ATCTAAAAGT CTATAAAGAA 3360
 TCAGATGCAT AGGCAATATG TTAAGTTCAC TTGGAGGCTA AAAATCTCCA GTGAAAACAA 3420
 AACGAAAACC TTTAAGAGAA TGTAAGATTT ATATAAACAC AAAGTATGCA TTGAAGATCT 3480
 GTTTCTACCA ATAAACATTA AAACAAAAAA AAAAAAAAAA AAAAAAA 3527

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Gln	Ser	Arg	Ser	Arg	Ser	Asp	Gly	Gly	Ser	Glu	Glu	Thr	Leu	1	5	10	15
Pro	Gln	Asp	His	Asn	His	His	Glu	Asn	Glu	Arg	Arg	Trp	Gln	Gln	Glu	20	25	30	
Arg	Leu	His	Arg	Glu	Glu	Ala	Tyr	Tyr	Gln	Phe	Ile	Asn	Glu	Leu	Asn	35	40	45	
Asp	Glu	Asp	Tyr	Arg	Leu	Met	Arg	Asp	His	Asn	Leu	Leu	Gly	Thr	Pro	50	55	60	
Gly	Glu	Ile	Thr	Ser	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Gly	Val	Lys	65	70	75	80
Glu	Gln	Leu	Ala	Ser	Gln	Pro	Asp	Leu	Arg	Asp	Gly	Thr	Asn	Tyr	Arg	85	90	95	
Asp	Ser	Glu	Val	Pro	Arg	Glu	Ser	Ser	His	Glu	Asp	Ser	Leu	Leu	Glu	100	105	110	
Trp	Leu	Asn	Thr	Phe	Arg	Arg	Thr	Gly	Asn	Ala	Thr	Arg	Ser	Gly	Gln	115	120	125	
Asn	Gly	Asn	Gln	Thr	Trp	Arg	Ala	Val	Ser	Arg	Thr	Asn	Pro	Asn	Asn	130	135	140	
Gly	Glu	Phe	Arg	Phe	Ser	Leu	Glu	Ile	His	Val	Asn	His	Glu	Asn	Arg	145	150	155	160
Gly	Phe	Glu	Ile	His	Gly	Glu	Asp	Tyr	Thr	Asp	Ile	Pro	Leu	Ser	Asp	165	170	175	
Ser	Asn	Arg	Asp	His	Thr	Ala	Asn	Arg	Gln	Gln	Arg	Ser	Thr	Ser	Pro	180	185	190	

Val Ala Arg Arg Thr Arg Ser Gln Thr Ser Val Asn Phe Asn Gly Ser
 195 200 205
 Ser Ser Asn Ile Pro Arg Thr Arg Leu Ala Ser Arg Gly Gln Asn Pro
 210 215 220
 Ala Glu Gly Ser Phe Ser Thr Leu Gly Arg Leu Arg Asn Gly Ile Gly
 225 230 235 240
 Gly Ala Ala Gly Ile Pro Arg Ala Asn Ala Ser Arg Thr Asn Phe Ser
 245 250 255
 Ser His Thr Asn Gln Ser Gly Gly Ser Glu Leu Arg Gln Arg Glu Gly
 260 265 270
 Gln Arg Phe Gly Ala Ala His Val Trp Glu Asn Gly Ala Arg Ser Asn
 275 280 285
 Val Thr Val Arg Asn Thr Asn Gln Arg Leu Glu Pro Ile Arg Leu Arg
 290 295 300
 Ser Thr Ser Asn Ser Arg Ser Arg Ser Pro Ile Gln Arg Gln Ser Gly
 305 310 315 320
 Thr Val Tyr His Asn Ser Gln Arg Glu Ser Arg Pro Val Gln Gln Thr
 325 330 335
 Thr Arg Arg Ser Val Arg Arg Arg Gly Arg Thr Arg Val Phe Leu Glu
 340 345 350
 Gln Asp Arg Glu Arg Glu Arg Arg Gly Thr Ala Tyr Thr Pro Phe Ser
 355 360 365
 Asn Ser Arg Leu Val Ser Arg Ile Thr Val Glu Glu Gly Glu Glu Ser
 370 375 380
 Ser Arg Ser Ser Thr Ala Val Arg Arg His Pro Thr Ile Thr Leu Asp
 385 390 395 400
 Leu Gln Val Arg Arg Ile Arg Pro Gly Glu Asn Arg Asp Arg Asp Ser
 405 410 415
 Ile Ala Asn Arg Thr Arg Ser Arg Val Gly Leu Ala Glu Asn Thr Val
 420 425 430
 Thr Ile Glu Ser Asn Ser Gly Gly Phe Arg Arg Thr Ile Ser Arg Leu
 435 440 445
 Glu Arg Ser Gly Ile Arg Thr Tyr Val Ser Thr Ile Thr Val Pro Leu
 450 455 460
 Arg Arg Ile Ser Glu Asn Glu Leu Val Glu Pro Ser Ser Val Ala Leu
 465 470 475 480
 Arg Ser Ile Leu Arg Gln Ile Met Thr Gly Phe Gly Glu Leu Ser Ser
 485 490 495

Leu Met Glu Ala Asp Ser Glu Ser Glu Leu Gln Arg Asn Gly Gln His
 500 505 510
 Leu Pro Asp Met His Ser Glu Leu Ser Asn Leu Gly Thr Asp Asn Asn
 515 520 525
 Arg Ser Gln His Arg Glu Gly Ser Ser Gln Asp Arg Gln Ala Gln Gly
 530 535 540
 Asp Ser Thr Glu Met His Gly Glu Asn Glu Thr Thr Gln Pro His Thr
 545 550 555 560
 Arg Asn Ser Asp Ser Arg Gly Gly Arg Gln Leu Arg Asn Pro Asn Asn
 565 570 575
 Leu Val Glu Thr Gly Thr Leu Pro Ile Leu Arg Leu Ala His Phe Phe
 580 585 590
 Leu Leu Asn Glu Ser Asp Asp Asp Arg Ile Arg Gly Leu Thr Lys
 595 600 605
 Glu Gln Ile Asp Asn Leu Ser Thr Arg His Tyr Glu His Asn Ser Ile
 610 615 620
 Asp Ser Glu Leu Gly Lys Ile Cys Ser Val Cys Ile Ser Asp Tyr Val
 625 630 635 640
 Thr Gly Asn Lys Leu Arg Gln Leu Pro Cys Met His Glu Phe His Ile
 645 650 655
 His Cys Ile Asp Arg Trp Leu Ser Glu Asn Cys Thr Cys Pro Ile Cys
 660 665 670
 Arg Gln Pro Val Leu Gly Ser Asn Ile Ala Asn Asn Gly
 675 680 685

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCCTGGGC TCCGCGCAGC CCACCGATCT GGGCGCCCAC AAGCGGCCGG CATCCGTGTC 60
 GAGCAGCGCT GCCGTGGAGC ACGAGCAGCG TGAGGCGGCA GCCAAGGAGA AACAACCGCC 120
 GCCGCCTGCG CACCGGGGCC CGGCCGACAG CCTGTCCACC GCGGCCGGGG CCGCCGAGCT 180

GAGCGCGGAA GGTGCGGGCA AGAGCCGCGG GTCTGGAGAG CAGGACTGGG TCAACAGGCC	240
CAAGACCGTG CGCGACACGC TGCTGGCGCT GCACCAGCAC GGCCACTCGG GGCCCTTCGA	300
GAGCAAGTTT AAGAAGGAGC CGGCCCTGAC TGCAGGCAGG TTGTTGGGTT TCGAGGCCAA	360
CGGGGCCAAC GGGTCTAAAG CAGTTGCAAG AACAGCAAGG AAAAGGAAGC CCTCTCCAGA	420
ACCAGAAGGT GAAGTCGGGC CCCCTAAGAT CAACGGAGAG GCCCAGCCGT GGCTGTCCAC	480
ATCCACAGAG GGGCTCAAGA TCCCCATGAC TCCTACATCC TCTTTTGTGT CTCCGCCACC	540
ACCCACTGCC TCACCTCATT CCAACCGGAC CACACGCGCT GAAGCGGCCC AGAATGGCCA	600
GTCCCCCATG GCAGCCCTGA TCTTAGTAGC AGACAATGCA GGGGGCAGTC ATGCCTCAAA	660
AGATGCCAAC CAGGTTCACT CCACTACCAG GAGGAATAGC AACAGTCCGC CCTCTCCGTC	720
CTCTATGAAC CAAAGAAGGC TGGGCCCCAG AGAGGTGGGG GGCCAGGGAG CAGGCAACAC	780
AGGAGGACTG GAGCCAGTGC ACCCTGCCAG CCTCCCGGAC TCCTCTCTGG CAACCAGTGC	840
CCCGCTGTGC TGCACCCTCT GCCACGAGCG GCTGGAGGAC ACCCATTTTG TGCAGTGCCC	900
GTCCGTCCCT TCGCACAAGT TCTGCTTCCC TTGCTCCAGA CAAAGCATCA AACAGCAGGG	960
AGCTAGTGGA GAGGTCTATT GTCCCAGTGG GGAAAAATGC CCTCTTGTGG GCTCCAATGT	1020
CCCCTGGGCC TTTATGCAAG GGGAAATTGC AACCATCCTT GCTGGAGATG TGAAAGTGAA	1080
AAAAGAGAGA GACTCGTGAC TTTTCCGGTT TCAGAAAAAC CCAATGATTA CCCTTAATTA	1140
AAACTGCTTG AATTGTATAT ATATCTCCAT ATATATATAT ATCCAAGACA AGGGAAATGT	1200
AGACTTCATA AACATGGCTG TATAATTTTG ATTTTTTTTG AATACATTGT GTTCTATAT	1260
TTTTTTTGAC GACAAAAGGT ATGTACTTAT AAAGACATTT TTTTCTTTTG TTAACGTTAT	1320
TAGCATATCT TTGTGCTTTA TTATCCTGGT GACAGTTACC GTTCTATGTA GGCTGTGACT	1380
TGCGCTGCTT TTTTAGAGCA CTTGGCAAAT CAGAAATGCT TCTAGCTGTA TTTGTATGCA	1440
CTTATTTTAA AAAAAAAAAA AAA	1463

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Thr Pro Thr Ser Ser Phe Val Ser Pro Pro Pro Pro Thr Ala Ser
1 5 10 15
Pro His Ser Asn Arg Thr Thr Pro Pro Glu Ala Ala Gln Asn Gly Gln
20 25 30
Ser Pro Met Ala Ala Leu Ile Leu Val Ala Asp Asn Ala Gly Gly Ser
35 40 45
His Ala Ser Lys Asp Ala Asn Gln Val His Ser Thr Thr Arg Arg Asn
50 55 60
Ser Asn Ser Pro Pro Ser Pro Ser Ser Met Asn Gln Arg Arg Leu Gly
65 70 75 80
Pro Arg Glu Val Gly Gly Gln Gly Ala Gly Asn Thr Gly Gly Leu Glu
85 90 95
Pro Val His Pro Ala Ser Leu Pro Asp Ser Ser Leu Ala Thr Ser Ala
100 105 110
Pro Leu Cys Cys Thr Leu Cys His Glu Arg Leu Glu Asp Thr His Phe
115 120 125
Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser
130 135 140
Arg Gln Ser Ile Lys Gln Gln Gly Ala Ser Gly Glu Val Tyr Cys Pro
145 150 155 160
Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe
165 170 175
Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys
180 185 190
Lys Glu Arg Asp Ser
195

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CATTTTTCTG	GTCCTTCTTA	AAAGTAATCA	CTCTTAAATT	TTGTGCTTAT	TCTGTTGTTT	60
TAAAAAATAG	TTTAAACAAA	TATGTGTGTA	CTCATAAACA	TAGGTTACTT	TTGCTTCTTT	120
TTGAGATATA	TTTAAATTTT	ATTGTGGTCT	ACATATTCTT	CAGCAGTTTG	TTTTTTTACC	180
CAATATTATG	TTTCATCTGT	ATTACTGCAT	TTACTATCCC	TAGTTGATTC	ACTTCCCTGA	240
AGTACAATAT	TCAGTTGTGT	GGCTATACCA	TAATTTAGTT	ATTCATTTTG	TTGTCAGTAA	300
AATTTGGGTG	ATTATCAGAT	TTTTTTCTAG	CATGAAAAAT	GCTACTARGA	ACATTCSTGT	360
ATGTGTCTAA	TGGTATACAC	TTTCAAGTGT	TTTTTTTATAT	ATGTGAGAGT	AGATTACTTG	420
GACCTTGAAG	ATGAACATGC	TATCTTTTCC	AGATACTGCC	AATTATTTCA	GCAAGATATG	480
AGTTCCCATC	ATTTTATATT	TGTCAGCATT	TGATATTTCC	AGGCCTAGTG	ATTTCCAGTC	540
ATTTACTGGA	TATAATATGA	TTATCTCTGT	AGGGAGTTGA	TTCCATCTC	CTCAATTACT	600
AATAAAGTTA	AAAATCTTTT	CATATGTTTT	ATTGCCATTT	TTATTTCTTC	TGTAAAGTAC	660
CTACTCATGG	CTTTTTCTCA	TTTTTTGTTT	GTCATCATTG	AATTATAGGA	GTTTTGAGAG	720
AGTGAGCAAG	CTAGTCTGTG	TGTGTGTGTG	TGTGCGTGTG	TGTGTATCTC	CTTAATGTGT	780
TATATGTGAT	TGGAACCTTCT	TCTCCACCT	TGATGCTTCC	TTCTTCCCC	ACTTGTTTTA	840
GGTATCTTCT	GATGAAGTGG	AGTTATTTAT	GGTATGTTCT	CAGGAGCTAC	AATTTTAAAT	900
TTCAATATAA	TCAGTGTTTT	TAATTATCTT	ATGTTTAGCT	CTTTTGGGTC	ATGCTTAGGA	960
AATTCTTCTT	AAATTTCAAT	GATAACAGTC	TTCCATACTT	TCTTCTAAAG	TCTTATATTT	1020
TGGCCTTTCA	TATTTATTCC	TTTAATCCAM	CTGGAGTAGA	TTTTTTTTTT	CCCTCTGTAG	1080
AGTTTGGAGT	AGAGATTTTA	TTTCCTTTTT	TTTTTTTTTT	TTTTTTTCTT	TTTTTTTGAG	1140
ACAGAGTCTT	GCTCTGTCGC	CCAGGCTGGA	GTGCAGTGGC	ACTATCTCAG	CTCACTGCAA	1200
CCTCCACCTC	CTGGGTTCOA	GCGATTCTCC	TGCCTCCGCC	TCCCGAGTAG	CTGGGACTAC	1260
AGGCATGTGC	CACCACGCCC	AGCTAATTTT	TTGTATTTTT	TTTAGTAGAG	ATGGGGTTCC	1320
ACCATGTTAG	CTAGGATGAT	TTCGATTTCC	TGACCTTGTG	ATCCGCCCCG	CTCGGCCTCC	1380
CAAAATGCTG	GGATTATAGG	TGTGAGCCAC	CACGTGGCCT	CATTTCATTC	TTTCATGTGG	1440
ATAGGCAGTT	GTTCCAGAAG	TATATAGTGA	GGAGCTTCTT	CTTTCTCTAA	TGATCTGCAA	1500
TGTCACCTTC	ATCATTTATG	AAGGTTGCAC	ATATACATGG	GAATTTTTTA	GTCTGGCATT	1560
AAATGTTCTT	CAAAAGAGTT	CCTGCAAACG	TTTTTGTTTT	TATTTCTTAC	TGTTCCCTTC	1620
ACGTACTCTC	TACTGAACTA	AACTCTGTAA	TGTGTCTCGA	AACTGTCCCA	CAATTTTCCT	1680

TGTCTTAAGA GTTTAATGCT TTCATACACC TCTCACATTC AGCCTTGTGC TATTGTCTTA 1740
 GGTATATTTA TTTCTCTTTT GCTCCCAATT ATGTTGTAAA CTTTTGGAAG CAGGAAGGAT 1800
 ATATTGTTCA TCTTTGGTAG CATTAAACAA TGAATACAGT GTTTTTTACT TAATAGATAT 1860
 TTGGTAAATC ATTGAACTAA ATTGGGGTTT GGAATTGAAG GTCTTAGAAA TTACCTGACC 1920
 ACTCCCATTA TATTTGCCCA TCCATGATCA CTGAGATTTA TAGAGATTAG ATGCAATGCC 1980
 CAGTTTCACA TATGTTTTTG CATCACTGTC TCTTTTTTTC TTGAGCTTAT TCCAGAGTGT 2040
 CTTTTAATAT CCATTCCATG ATCAAATGGC TGAACTATTA AAATGCTGTC CAGAAGTGTA 2100
 AAGCAATATG AAGATGCTAG AAAAGTTGAA GAGACACATA TATGGTAGGT CCAAGACCAT 2160
 TACACTTACT GAGTCCATTA CTAAAAATGA TGTTCACCTA ACATCAAAAC ACTCAGGATT 2220
 ACCCAAGCAC AATATACTGA TTTGCACCTC TGCCTTTGTT CATGCCCTT GTTCAGGAGA 2280
 ACTGCTTTCA TGTGCTACTG TCCATAGATC TTCTCTATCC TTACAGATTA ATTTCTTCCT 2340
 TTTGAATGCT ATGTTTCCAT ACTTTGACAT TCCTTCTGCA CCATTCAGAC CATATTTTAG 2400
 TTCTTTTTTA TGGTATCTCT CACTTTTGAT TGTCACCCCT TAAGTCAAAG ACAATTTTTT 2460
 CATCTGTGTC TTCTCAACAC CCAGCACAGG GCTATGTTTG GTAAAAATTA GGTATCCAAG 2520
 ATGTACTAAA TGAAAAAAAA AAAAAAA 2547

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Phe	Phe	Lys	Arg	Val	Pro	Ala	Asn	Val	Phe	Val	Phe	Ile	Ser	Tyr
1				5					10					15	
Cys	Ser	Leu	His	Val	Leu	Ser	Thr	Glu	Leu	Asn	Ser	Val	Met	Cys	Leu
			20					25					30		
Glu	Thr	Val	Pro	Gln	Phe	Ser	Leu	Ser							
		35					40								

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTCAACGGC CTCTTCTGGT TGCTGTCTTC CTCGTCCCTC CGGCCCTTCT TCCTACTCAG	60
CGTCTCACTT TTGGCCTATT TTCTGCTGGA TCTCTGGCAG CCTCGCTTTC TCCCTGACGT	120
TTCAGCATCA TCCCCAGAGG AGCCCACTC TGACAGTGAG GGTGCGGGGT CAGGCGCCCG	180
GCCGCACCTG CTGAGTGTGC CCGAGTTGTG CAGATACCTG GCTGAGAGCT GGCTCACCTT	240
CCAGATTCAC CTGCAGGAGC TGCTGCAGTA CAAGAGGCAG AATCCAGCTC AGTTCTGCGT	300
TCGARTCTGC TCTGGCTGTG CTGTGTTGGC TGTGTTGGGA CACTATGTTT CAGGGATTAT	360
GATTTCTAC ATTGTCTTGT TGAGTATCCT GCTGTGGCCC CTGGTGGTTT ATCATGARCT	420
GATCCAGAGG ATGTWCACTC GCCTGGAGCC CCTGCTCATG CAGCTGGACT ACAGCATGAA	480
GGCAGAAKCC AATGCCCTGC ATCACAAACA CGACAAGAGG AAGCGTCAGG GGAAGAATGC	540
ACCCCCAGGA GGTGATGAGC CACTGGCAGA GACAGAGAGT GAAAGCGAGG CAGAGCTGGC	600
TGGCTTCTCC CCAGTGGTGG ATGTGAAGAA AACAGCATTG GCCTTGGCCA TTACAGACTC	660
AGAGCTGTCA GATGAGGAGG CTTCTATCTT GGAGAGTGGT GGCTTCTCCG TATCCCGGGC	720
CACAACTCCG CAGCTGACTG ATGTCTCCGA GGATTTGGAC CAGCAGAGCC TGCCAAGTGA	780
ACCAGAGGAG ACCCTAAGCC GGGACCTAGG GGAGGGAGAG GAGGGAGAGC TGGCCCCCTCC	840
CGAAGACCTA CTAGGCCGTC CTCAAGCTCT GTCAAGGCAA GCCCTGGACT TGGAGGAAGA	900
GGAAGAGGAT GTGGCAGCTA AGGAAACCTT GTTGC GGCTC TCATCCCCC TCCACTTTGT	960
GAACACGCAC TTCAATGGGG CAGGGTCCCC CCCAGATGGA GTGAAATGCT CCCCTGGAGG	1020
ACCAGTGGAG AACTGAGCC CCGAGACAGT GAGTGGTGGC CTCACTGCTC TGCCCGGCAC	1080
CCTGTCACCT CCACTTTGCC TTGTTGGAAG TGACCCAGCC CCCTCCCCTT CCATTCTCCC	1140
ACCTGTTCCC CAGGACTCAC CCCAGCCCCT GCCTGCCCCCT GAGGAAGAAG AGGCACTCAC	1200
CACTGAGGAC TTTGAGTTGC TGGATCAGGG GGAGCTGGAG CAGCTGAATG CAGAGCTGGG	1260
CTTGAGCCA GAGACACCGC CAAAACCCCC TGATGCTCCA CCCCTGGGGC CCGACATCCA	1320
TTCTCTGGTA CAGTCAGACC AAGAAGCTCA GGCCGTGGCA GAGCCATGAG CCAGCCGTTG	1380

AGGAAGGAGC TGCAGGCACA GTAGGGCTTC CTGGCTAGGA GTGTTGCTGT TTCCTCCTTT	1440
GCCTACCACT CTGGGGTGGG GCAGTGTGTG GGGAAGCTGG CTGTCGGATG GTAGCTATTG	1500
CACCYTCTGC CTGCCTGCCT GCCTGCTGTC CTGGGCATGG TGCAGTACCT GTGCCTAGGA	1560
TTGGTTTTAA ATTTGTAAAT AATTTTCCAT TTGGGTTAGT GGATGTGAAC AGGGCTAGGG	1620
AAGTCCTTCC CACAGCCTGC GCTTGCCTCC CTGCCTCATC TCTATTCTCA TTCCACTATG	1680
CCCCAAGCCC TGGTGGTCTG GCCCTTTCTT TTTCTCCTA TCCTCAGGGA CCTGTGCTGC	1740
TCTGCCCTCA TGTCCCACTT GGTGTGTTAG TTGAGGCACT TTATAATTTT TCTCTTGTCT	1800
TGTGTTCCCTT TCTGCTTTAT TTCCCTGCTG TGTCTGTCC TTAGCAGCTC AACCCCATCC	1860
TTTGCCAGCT CCTCCTATCC CGTGGGCACT GGCCAAGCTT TAGGGAGGCT CCTGGTCTGG	1920
GAAGTAAAGA GTAAACCTGG GGCAGTGGGT CAGGCCAGTA GTTACACTCT TAGGTCACTG	1980
TAGTCTGTGT AACCTTCACT GCATCCTTGC CCCATTCAGC CCGGCCTTTC ATGATGCAGG	2040
AGAGCAGGGA TCCCGCAGTA CATGGCGCCA GCACTGGAGT TGGTGAGCAT GTGCTCTYTY	2100
TTGAGATTAG GAGCTTCCTT ACTGCTCCTC TGGGTGATCC AAGTGTAGTG GGACCCCTA	2160
CTAGGGTCAG GAAGTGGACA CTAACATCTG TGCAGGTGTT GACTTGAAAA ATAAAGTGTT	2220
GATTGGCTAG AAAAAAAAAA AAAAA	2245

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ile	Ser	Tyr	Ile	Val	Leu	Leu	Ser	Ile	Leu	Leu	Trp	Pro	Leu	Val
1				5				10					15		
Val	Tyr	His	Glu	Leu	Ile	Gln	Arg	Met	Xaa	Thr	Arg	Leu	Glu	Pro	Leu
			20				25					30			
Leu	Met	Gln	Leu	Asp	Tyr	Ser	Met	Lys	Ala	Glu	Xaa	Asn	Ala	Leu	His
		35				40						45			
His	Lys	His	Asp	Lys	Arg	Lys	Arg	Gln	Gly	Lys	Asn	Ala	Pro	Pro	Gly
	50				55					60					
Gly	Asp	Glu	Pro	Leu	Ala	Glu	Thr	Glu	Ser	Glu	Ser	Glu	Ala	Glu	Leu
65				70				75						80	

Ala Gly Phe Ser Pro Val Val Asp Val Lys Lys Thr Ala Leu Ala Leu
 85 90 95
 Ala Ile Thr Asp Ser Glu Leu Ser Asp Glu Glu Ala Ser Ile Leu Glu
 100 105 110
 Ser Gly Gly Phe Ser Val Ser Arg Ala Thr Thr Pro Gln Leu Thr Asp
 115 120 125
 Val Ser Glu Asp Leu Asp Gln Gln Ser Leu Pro Ser Glu Pro Glu Glu
 130 135 140
 Thr Leu Ser Arg Asp Leu Gly Glu Gly Glu Glu Gly Glu Leu Ala Pro
 145 150 155 160
 Pro Glu Asp Leu Leu Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu
 165 170 175
 Asp Leu Glu Glu Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu
 180 185 190
 Arg Leu Ser Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala
 195 200 205
 Gly Ser Pro Pro Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu
 210 215 220
 Thr Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly
 225 230 235 240
 Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro Ser
 245 250 255
 Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro Leu Pro
 260 265 270
 Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe Glu Leu Leu
 275 280 285
 Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu Gly Leu Glu Pro
 290 295 300
 Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro Leu Gly Pro Asp Ile
 305 310 315 320
 His Ser Leu Val Gln Ser Asp Gln Glu Ala Gln Ala Val Ala Glu Pro
 325 330 335

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGTGGGAA GAGCTGAAGC AGGCGCTCTT GGCTCGGCGC GGCCCGCTGC AATCCGTGGA	60
GGAACGCGCC GCCGAGCCAC CATCATGCCT GGGCACTTAC AGGAAGGCTT CGGCTGCGTG	120
GTCACCAACC GATTTCGACCA GTTATTTGAC GACGAATCGG ACCCCTTCGA GGTGCTGAAG	180
GCAGCAGAGA ACAAGAAAAA AGAAGCCGGC GGGGGCGGCG TTGGGGGCCC TGGGGCCAAG	240
AGCGCAGCTC AGGCCGCGGC CCAGACCAAC TCCAACGCGG CAGGCAAACA GCTGCGCAAG	300
GAGTCCCAGA AAGACCGCAA GAACCCGCTG CCCCCAGCG TTGGCGTGGT TGACAAGAAA	360
GAGGAGACGC AGCCGCCCCG GCGCTTAAG AAAGAAGGAA TAAGACGAGT TGGGAAGAAGA	420
CCTGATCAAC AACTTCAGGG TGAAGGGAAA ATAATTGATA GAAGACCAGA AAGGCGACCA	480
CCTCGTGAAC GAAGATTCTGA AAAGCCACTT GAAGAAAAGG GTGAAGGAGG CGAATTTTCA	540
GTTGATAGAC CGATTATTGA CCGACCTATT CGAGGTCGTG GTGGTCTTGG AAGAGGTCGA	600
GGGGGCCGTG GACGTGGAAT GGGCCGAGGA GATGGATTTG ATTCTCGTGG CAAACGTGAA	660
TTTGATAGGC ATAGTGGAAG TGATAGATCT TCTTTTTCAC ATTACAGTGG CCTGAAGCAC	720
GAGGACAAAC GTGGAGGTAG CGGATCTCAC AACTGGGGAA CTGTCAAAGA CGAATTAACT	780
GACTTGATC AATCAAATGT GACTGAGGAA ACACCTGAAG GTGAAGAACA TCATCCAGTG	840
GCAGACACTG AAAATAAGGA GAATGAAGTT GAAGAGGTAA AAGAGGAGGG TCCAAAAGAG	900
ATGACTTTGG ATGAGTGGA GGTATTCAA AATAAGGACC GGCAAAAGT AGAATTTAAT	960
ATCCGAAAAC CAAATGAAGG TGCTGATGGG CAGTGAAGA AGGGATTTGT TCTTCATAAA	1020
TCAAAGAGTG AAGAGGCTCA TGCTGAAGAT TCGGTTATGG ACCATCATTT CCGGAAGCCA	1080
GCAAATGATA TAACGTTTCA GCTGGAGATC AATTTTGGAG ACCTTGCCG CCCAGGACGT	1140
GGCGGCAGGG GAGGACGAGG TGGACGTGGG CGTGGTGGGC GCCCAAACCG TGGCAGCAGG	1200
ACCGACAAGT CAAGTGCTTT TGCTCCTGAT GTGGATGACC CAGAGGCATT CCCAGTTTGT	1260
GCTTAAMTGG ATGCCATAAG ACAACCCTGG TTCCTTTGTG AACCCTTTTG TTCAAAGCTT	1320
TTGCATGCTT AAGGATTCCA AACGACTAAG AAATTAAAAA AAAAAAAAAA AAAAAAAAAA	1380
AAAAAAAAA AAAAAAAAAA AAAAAA	1406

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Pro	Gly	His	Leu	Gln	Glu	Gly	Phe	Gly	Cys	Val	Val	Thr	Asn	Arg	
1				5					10					15		
Phe	Asp	Gln	Leu	Phe	Asp	Asp	Glu	Ser	Asp	Pro	Phe	Glu	Val	Leu	Lys	
			20					25					30			
Ala	Ala	Glu	Asn	Lys	Lys	Lys	Glu	Ala	Gly	Gly	Gly	Gly	Val	Gly	Gly	
			35				40						45			
Pro	Gly	Ala	Lys	Ser	Ala	Ala	Gln	Ala	Ala	Ala	Gln	Thr	Asn	Ser	Asn	
	50					55					60					
Ala	Ala	Gly	Lys	Gln	Leu	Arg	Lys	Glu	Ser	Gln	Lys	Asp	Arg	Lys	Asn	
65					70					75					80	
Pro	Leu	Pro	Pro	Ser	Val	Gly	Val	Val	Asp	Lys	Lys	Glu	Glu	Thr	Gln	
				85					90					95		
Pro	Pro	Val	Ala	Leu	Lys	Lys	Glu	Gly	Ile	Arg	Arg	Val	Gly	Arg	Arg	
			100					105					110			
Pro	Asp	Gln	Gln	Leu	Gln	Gly	Glu	Gly	Lys	Ile	Ile	Asp	Arg	Arg	Pro	
		115					120					125				
Glu	Arg	Arg	Pro	Pro	Arg	Glu	Arg	Arg	Phe	Glu	Lys	Pro	Leu	Glu	Glu	
	130					135					140					
Lys	Gly	Glu	Gly	Gly	Glu	Phe	Ser	Val	Asp	Arg	Pro	Ile	Ile	Asp	Arg	
145					150					155					160	
Pro	Ile	Arg	Gly	Arg	Gly	Gly	Leu	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Gly	
				165					170					175		
Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser	Arg	Gly	Lys	Arg	Glu	
			180					185					190			
Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Ser	Phe	Ser	His	Tyr	Ser	
		195					200					205				
Gly	Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	
	210					215					220					
Gly	Thr	Val	Lys	Asp	Glu	Leu	Thr	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	
225					230					235					240	

Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr Glu
 245 250 255
 Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys Glu
 260 265 270
 Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala Lys
 275 280 285
 Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln Trp
 290 295 300
 Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His Ala
 305 310 315 320
 Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp Ile
 325 330 335
 Thr Phe Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly Arg
 340 345 350
 Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Gly Arg Pro Asn
 355 360 365
 Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Phe Ala Pro Asp Val Asp
 370 375 380
 Asp Pro Glu Ala Phe Pro Val Leu Ala
 385 390

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGACGCGG CCAGTCAGGT GCTCCTGGGC TCCGGTCTCA CCATCCTGTC CCAGCCGCTC 60
 ATGTACGTGA AAGTGCTCAT CCAGGTGGGA TATGAGCCTC TTCCTCCAAC AATAGGACGA 120
 AATATTTTGT GCGGCAAGT GTGTCAGCTT CCTGGTCTCT TTAGTTATGC TCAGCACATT 180
 GCCAGTATCG ATGGGAGGCG CGGGTTGTTC ACAGGCTTAA CTCCAAGACT GTGTTCGGGA 240
 GTCCTTGGA CTGTGGTCCA TGGTAAAGTT TTACAGCATT ACCAGGAGAG TGACAAGGGT 300
 GAGGAGTTAG GAMCTGAAAA TGTACARAAA GAAGTCTCAT CTTCTTTGA MCACGTTATC 360

AAGGAGACAA CTCGAGAGAT GATCGCTCGT TCTGCTGCTA CCCTCATCAC ACATCCCTTC	420
CATGTTGATC ACTCTGAGAT CTATGGTACA RTTCATTGGC AGAGAATCCA AGTACTGTGG	480
ACTTTGTGAT TCCATAATAA CCATCTATCG GGAAGAGGGC ATTCTAGGAT TTTTCGCGGG	540
TCTTGTTCCCT CGCCTTCTAG GTGACATCCT TTCTTTGTGG CTGTGTAAC TACTGGCCTA	600
CCTCGTCAAT ACCTATGCAC TGGACAGTGG GGTTCCTACC ATGAATGAAA TGAAGAGTTA	660
TTCTCAAGCT GTCACAGGAT TTTTGGCGAG TATGTTGACC TATCCCTTTG TGCTTGTCTC	720
CAATCTTATG GCTGTCAACA ACTGTGGTCT TGCTGGTGGA TGCCCTCCTT ACTCCCCAAT	780
ATATACGTCT TGGATAGACT GTTGGTGCAT GCTACAAAAA GAGGGGAATA TGAGCCGAGG	840
AAATAGCTTA TTTTCCGGA AGGTCCCCTT TGGGAAGACT TATTGTTGTG ACCTGAAAAAT	900
GTTAATTTGA AGATGTGGGG CAGGGACAGT GACATTTCTG TAGTCCCAGA TGCACAGAAT	960
TATGGGAGAG AATGTTGATT TCTATACAGT GTGGCGCGCT TTTTAAATAA TCATTTAATC	1020
TTGGGAAAAAT TCAGGTGTTT GGTGTCTGCC TTTTGTTC TTTTTCAG CACAACATAA	1080
CTTACCACTG AACTCCCC TTTAGTTATT CTGAATTAGG ATATTTTGC TCCAAATTCT	1140
TATTTTACTT AACCAGAAGG GAAAAAAGT TGTATTTCC TGAAGCTACA GGCACTTTGT	1200
CATGTGATTT TTGAGTCTCA ATTTAAGGCT TTGTAAAATG AAGAGTAGAA TTCCAAGAAA	1260
AATGAGAAAT AATTTTGTA AACTTAACAA AATCACTAAA TTAACTATA TGGGAGGTTA	1320
TGAATTACTT TTTCTGGGT AGACCCTAAA ATGTCAGTAG CATGCACCAG AATCTGACTC	1380
CCATTATGCT TCTAAGCACA TTTCAATTGAC CTTGTCTCTC AACTTCAAG AAAAGGACAG	1440
TACATTGCTA CATTACCCTA GAAAGTCTGT GTGAGGATCT GCCCCTTCAG TCTGTTATTG	1500
CAAAGTAATA AAATGTCACC TACAGGGAGC CTCTGAGCCT ACTCTAGTTC AAGAGGCTAC	1560
CTGAAAAAAA ATAAATAAGA TAAAGGGTCA GCAACAACAA AGAAAAAGAC AATTACAGAA	1620
AATAAGCAAG ATTTGGAAAG GAAGTATAAT GGCACTTTTT TCCTCAAAGG AAGTTCTTGT	1680
TTTCACATAA AATATGAAAA GCAGATCCTG CAGGAGTAAC CCCCTTCTTT AAGAGCCAAG	1740
TATTTGCCAG TGCTTAAATT ACACCATACC GTTCTAATTA TATATAATCT TTTGTTCTTC	1800
AGTTTTTTGT TTTGTTTCCT TTTGTTATT GTTGCCGAAG GTGAGTAGTT TTGCATTTCT	1860
GATGACAGCC TTGGAAAGTA TATTTGTAAC TCCATGTCTG GTAATGCCAA CCCAAGTCGA	1920
CATGGGTCTT AGGACACTGA CCACCTCACA TGCCATACCC TCAGTTAAGC ATGTTAACAT	1980
TTATAGGAGG AAAAAAATCA CTTTGGGAGA AAATAAAATT CAACTCAAGC ATAAAGCTTC	2040
TGTTTACTCA GGCCTTCTAA AAAGCAGGTT AAAATGCTCT AAAATGAGAA AGCCTGTGGT	2100

TTCAC TTATT	TATATAACTC	ACTGGGACAT	TGCCAAATGA	GTAAGCACTT	AATTCGCTGC	2160
TTCTGAGACT	TCTCTGTCAA	AACAGCCCCA	CTGATAATAT	TAGACAGAAC	GAGAATGCAG	2220
GGGTCTCTTC	CCTCCCCTGG	GGTTTAGGAA	GCTCATGAGG	AGCTCGGCTT	AAAATGTCTT	2280
TGATGTCTCT	TCCTTTGTCT	CAAAAAGTAA	TGTCAATTTT	ATATACTATT	TCAATATTAC	2340
TATCTGCATT	TGTTTTAATA	TAAAAATGTT	TGCTGCCTAC	CTTTTTCTCC	CAAAAAATCT	2400
TTAAGTAAAG	ATGATCTGGG	AAAATGAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2460
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2520
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2580
AAAAAAAAAA	AAAAAAAAGC	GGCCGCAGGT	CTAGAATTCA	ATCGGAAGGT	ATATAGCTTA	2640
TTTGTGTGCTT	TTCATTGTAA	TTTAACATGG	TTAATGGTTA	ATTACTATTT	AACACACATT	2700
TCAAATGAAT	ATTATTTGGG	GGATTAGATT	GAGTGAAATT	AACCTGCTAT	TAAATAGTAA	2760
ACTTTTCCTC	TGGAGTCACT	TTTTTCCCCC	TTCAAAGTAT	GTTACTGAGG	AAGTAAACTT	2820
TTTTTTTTTT	TTTTGGTTTT	TGTTTTTTGA	GACACAGTCT	CGCTCTGTTG	CCCAGGCTGC	2880
TGGAGTGCCG	TGGCGCAATC	TCGGCTCACT	GCAACCTCCG	CCTCCTGGAT	TCAAACAATT	2940
CTCCTGCTTC	AGCCTCCTGA	GTAGCTGGGA	TTACAGGCAC	ATGCCACCAC	GCCCCGCTAA	3000
TTTTTGATAT	TTTAGTAGAG	ACTGGGTTTC	ACCATGTTGG	TCAGGCTGGT	CTCAAACCTC	3060
TGACCTCGTG	ATCCACCCGC	CTCGGCCTCC	CAAAATCCTG	GGATTACAGG	CGCGAGCCAC	3120
CACACCCGGC	TGGAAGTAAA	CATTTTTTAA	GCTACTTTTA	CTCATTTCTAG	CCTTGTTAGAA	3180
TGACCATTGC	AGCTTGAGGG	ACCTAGTTCT	TACCTTTTCT	TGCAACCAAC	ACACTTGCAA	3240
TTGTGTCTGG	TATGCTTGTT	CCTGCTGCTA	ATAAAGTAAG	GCCCATTACT	GTATCGGGAA	3300
TTTCTAGTGT	TTCCCCTGTA	ATAAACAGAT	ATTTCAAGTT	ACAAATCTTA	AAGATTCACT	3360
AACCATCCTT	TGCAGTTATT	TTGGATATTT	CCTTCGTGAA	CAAAAATAAA	ATAGGCACAT	3420
TTAGAATTCA	GAGCCAATAT	GTGCTTGCTT	ATTAGTTTTT	TAGCTAGCAA	CATATTTGAA	3480
TCAGGCTGGT	AATTCGGGTA	ACCCAGGTAG	CACAGATTTT	TAATGACATA	TYTAAAGATA	3540
CGTAACAGCT	AAAATTTCTG	CCAGTGAGAA	ATTTTCCTGT	TTGATATTTT	TTACAAAAGA	3600
TGTTTATGTC	CACCATTATY	TTCATTCAGG	GGCTGTGCTG	AATATTTGAT	AATGAGACTG	3660
ATCATTCGCG	TTTTTCTTTC	TTAAAAATAT	TAGGCAGAGT	TAAGCAAATT	AATTATAGCT	3720
ATCTTTAAGC	TATAAATGTG	TTAACATGTA	TATATACCAT	TTATTATGTT	CTACTTTAGT	3780

GATATACCTT AATTAGTGG GCTTTGGCAG GCGGGGGGAG GGGGAACGTT CATTAATCTC	3840
TGAGGAAAAAC AAAACCTGTT TTCTACTTGA GTCTAACATA TGGTCCCAAT TTATTAATAC	3900
TTCTGTAAAA TTTGATGTCA GGTCAACATT TTTCAGAAAT GTATTTATTC TCAGAAACAG	3960
AACCAGAGAG AAGTTAAACA AAAGGTTATG TAACTGTTCC TTTAATGTTG TAATTGAAAA	4020
CTTGGTTTAG CGTCTTTTTT TTCTTTCTCT TTTTTTTTCT TAAAATGCCA ACTAAAATAA	4080
TTAGAAAAGTA GCTTATTTAT TGCATGCTTA TACATTGATA TTGGAATTGG AATTGGTTGT	4140
TAATTTCTGT TACTGGCTTT GCTAGAATTC ATATGTGCAT AAATAACACT AATATTTATC	4200
ATCTTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA	4237

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Tyr	Ile	Tyr	His	Leu	Leu	Cys	Ser	Thr	Leu	Val	Ile	Tyr	Leu	Asn
1				5				10					15		
Leu	Val	Gly	Phe	Gly	Arg	Ala	Gly	Glu	Gly	Glu	Arg	Ser	Leu	Ile	Ser
		20					25						30		
Glu	Glu	Asn	Lys	Thr	Cys	Phe	Leu	Leu	Glu	Ser	Asn	Ile	Trp	Ser	Gln
		35					40					45			
Phe	Ile	Asn	Thr	Ser	Val	Lys	Phe	Asp	Val	Arg	Ser	Thr	Phe	Phe	Arg
	50					55				60					
Asn	Val	Phe	Ile	Leu	Arg	Asn	Arg	Thr	Arg	Glu	Lys	Leu	Asn	Lys	Arg
65				70					75					80	
Leu	Cys	Asn	Cys	Ser	Phe	Asn	Val	Val	Ile	Glu	Asn	Leu	Val		
			85						90						

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TNTTGAAGACT GTTGCTTGTT TGGAATGT

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CNCCATCTAAT GGGATGATGG GTTCTTGA

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANTTTCCGTCA CCTCGTTCGC CTGCTGCT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GNATACGAGGG GTTCCCATGG CTTCTTCT

29

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TNTACGACGAC ATCCAACAAT CACACTGG

29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNGTCCGGTTG GAATGAGGTG AGGCAGTG

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNTCCTCACTA TATACTTCTG GAACAACT

29

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCCTAAGAGT GTAACTACTG GCCTGACC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNTCCTCGTGC TTCAGGCCAC TGTAATGT

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ANGCCCACTAA ATTAAGGTAT ATCACTAA

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Trp Gly Leu Gly Thr Thr Ser Ser Phe Arg Trp Tyr Ser Ser Asp

1	5	10	15
Tyr Arg Arg Ser Phe Gln Leu Asn Ser Pro Val Asp Lys Met Arg Lys			
20	25	30	
Thr Gly Glu Gln Ala Phe Ser Val Phe Thr Tyr Lys Val Arg Ser Val			
35	40	45	
Met Gly Gln			
50			

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO33:

AGTTGGCAGG TGGAGAGGCA GGTTGGGAGG GAAAGTCGGG GGAGGACGCG GAAGAGGAGC	60
TGTGGGAAGG GGGAGGAGGG AGGGAGGAAA AGAGGAGGAG GCGGAGGAGA ACTGAGCAGA	120
GCAGAGCATC GAGCCAAAGG GGAGATGAGT TTGTCTGTCC TCTGCTGAGG CTACGGCCGG	180
GCCTAGGGAA CTGGGAGCTT GGGTGAAGC GACACCCGTG GAAGTGGGAG GAGGTGGCGC	240
CGGGACTTTA ACCCCTTG TG GCTCTGCGG CAGGGGATTT AACCCTTTGT GGATCTGGCC	300
CCTCGGAGGC AGCGTCATCG GTAGTTTTAA CCCCTTCGGG GCTGGGTTC ACGCACTGGA	360
CTTACCCTCA TCACCTTGCT CACCAACTCC TTTATTGGGG TGCTCCGCTT GGAGGTTTGA	420
GGCCACCTC CGCCATTAC GTACTGTTCC TGCCGCTGCA CCCCCTTGGA CCCGCTAGCT	480
GGCCGCACTG TGGGCGCTTA ACCCTTTACT GACTTGAGCT CCCAGATTG CAGTTGGAGT	540
TTGCTGATAG AAGGACTAGC TAAAGGCGTC ACTGCAGGAA TTACAACTG AAGAGGACTC	600
TGTTGGACTG TTTTTTTTTT CTTTTTCTTT TTTTAAAGAA AAACCCATTT TTTTCCTTAA	660
GGACTTACTA GCCAAAATTT CTAAACTTC GAGGACTCTA CTAGCCATGG CCGAGCCATT	720
CTTGTCAGAA TATCAACACC AGCCTCAAAC TAGCAACTGT ACAGGTGCTG CTGCTGTCCA	780
GGAAGAGCTG AACCTGAGC GCCCCCAGG CGCGGAGGAG CGGGTGCCCG AGGAGGACAG	840
TAGGTGGCAA TCGAGAGCGT TCCCCAGTT GGGTGGCCGT CCGGGGCCGG AGGGGGAAGG	900
GAGCCTGGAA TCCCAACCAC CTCCCTTGCA GACCCAGGCC TGTCCAGAAT CTAGCTGCCT	960

GAGAGAGGGC	GAGAAGGGCC	AGAATGGGGA	CGACTCGTCC	GCTGGCGGCG	ACTTCCCGCC	1020
GCCGGCAGAA	GTGGAACCGA	CGCCCGAGGC	CGAGCTGCTC	GCCCAGCCTT	GTCATGACTC	1080
CGAGGCCAGT	AAGTTGGGGG	CTCCTGCCGC	AGGGGGCGAA	GAGGAGTGGG	GACAGCAGCA	1140
GAGACAGCTG	GGGAAGAAAA	AACATAGGAG	ACGCCCCTCC	AAGAAGAAGC	GGCATTGGAA	1200
ACCGTACTAC	AAGCTGACCT	GGGAAGAGAA	GAAAAAGTTC	GACGAGAAAC	AGAGCCTTGC	1260
AGCTTCAAGG	ATCCGAGCCG	AGATGTTCGC	CAAGGGCCAG	CCGGTCGCGC	CCTATAACAC	1320
CACGCAGTTC	CTCATGGATG	ATCACGACCA	GGAGGAGCCG	GATCTCAAAA	CCGGCCTGTA	1380
CTCCAAGCGG	GCCGCCGCCA	AATCCGACGA	CACCAGCGAT	GACGACTTCA	TGGAAGAAGG	1440
GGGTGAGGAG	GATGGGGGCA	GCGATGGGAT	GGGAGGGGAC	GGCAGCGAGT	TTCTGCAGCG	1500
GGACTTCTCG	GAGACGTACG	AGCGGTACCA	CACGGAGAGC	CTGCAGAACA	TGAGCAAGCA	1560
GGAGCTCATC	AAGGAGTACC	TGGAAGTGGG	GAAGTGCCCTC	TCGCGCATGG	AGGACGAGAA	1620
CAACCGGCTG	CGGCTGGAGA	GCAAGCGGCT	GGGTGGCGAC	GACGCGCGTG	TGCGGGAGCT	1680
GGAGCTGGAG	CTGGACCGGC	TGCGCGCCGA	GAACCTCCAG	CTGCTGACCG	AGAACGAACT	1740
GCACCGGCAG	CAGGAGCGAG	CGCCGCTTTC	CAAGTTTGGA	GACTAGACTG	AAACTTTTTT	1800
GGGGGAGGGG	GCAAAGGGGA	CTTTTACAG	TGATGGAATG	TAACATTATA	TACATGTGTA	1860
TATAAGACAG	TGGACCTTTT	TATGACACAT	AATCAGAAGA	GAAATCCCCC	TGGCTTTGGT	1920
TGGTTTCGTA	AATTTAGCTA	TATGTAGCTT	GCGTGCTTTC	TCCTGTTCTT	TTAATTATGT	1980
GAAACTGAAG	AGTTGCTTTT	CTTGTTTTC	TTTTTAGAAG	TTTTTTTCCT	TAATGTGAAA	2040
GTAATTTGAC	CAAGTTATAA	TGCATTTTTG	TTTTTAACAA	ATCCCCTCCT	TAAACGGAGC	2100
TATAAGGTGG	CCAAATCTGA	GAACAATTAA	ATTCATTTTA	GTTATAATAA	ATTTAATATT	2160
TGTAAATGTA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA			2199

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Glu Pro Phe Leu Ser Glu Tyr Gln His Gln Pro Gln Thr Ser

1		5		10		15											
Asn	Cys	Thr	Gly	Ala	Ala	Ala	Val	Gln	Glu	Glu	Leu	Asn	Pro	Glu	Arg		
			20					25					30				
Pro	Pro	Gly	Ala	Glu	Glu	Arg	Val	Pro	Glu	Glu	Asp	Ser	Arg	Trp	Gln		
		35					40					45					
Ser	Arg	Ala	Phe	Pro	Gln	Leu	Gly	Gly	Arg	Pro	Gly	Pro	Glu	Gly	Glu		
	50					55					60						
Gly	Ser	Leu	Glu	Ser	Gln	Pro	Pro	Pro	Leu	Gln	Thr	Gln	Ala	Cys	Pro		
65					70					75					80		
Glu	Ser	Ser	Cys	Leu	Arg	Glu	Gly	Glu	Lys	Gly	Gln	Asn	Gly	Asp	Asp		
				85					90					95			
Ser	Ser	Ala	Gly	Gly	Asp	Phe	Pro	Pro	Pro	Ala	Glu	Val	Glu	Pro	Thr		
			100					105					110				
Pro	Glu	Ala	Glu	Leu	Leu	Ala	Gln	Pro	Cys	His	Asp	Ser	Glu	Ala	Ser		
		115					120					125					
Lys	Leu	Gly	Ala	Pro	Ala	Ala	Gly	Gly	Glu	Glu	Glu	Trp	Gly	Gln	Gln		
	130					135						140					
Gln	Arg	Gln	Leu	Gly	Lys	Lys	Lys	His	Arg	Arg	Arg	Pro	Ser	Lys	Lys		
145					150					155					160		
Lys	Arg	His	Trp	Lys	Pro	Tyr	Tyr	Lys	Leu	Thr	Trp	Glu	Glu	Lys	Lys		
				165					170					175			
Lys	Phe	Asp	Glu	Lys	Gln	Ser	Leu	Arg	Ala	Ser	Arg	Ile	Arg	Ala	Glu		
			180					185					190				
Met	Phe	Ala	Lys	Gly	Gln	Pro	Val	Ala	Pro	Tyr	Asn	Thr	Thr	Gln	Phe		
		195					200					205					
Leu	Met	Asp	Asp	His	Asp	Gln	Glu	Glu	Pro	Asp	Leu	Lys	Thr	Gly	Leu		
	210					215					220						
Tyr	Ser	Lys	Arg	Ala	Ala	Ala	Lys	Ser	Asp	Asp	Thr	Ser	Asp	Asp	Asp		
225					230					235					240		
Phe	Met	Glu	Glu	Gly	Gly	Glu	Glu	Asp	Gly	Gly	Ser	Asp	Gly	Met	Gly		
				245					250					255			
Gly	Asp	Gly	Ser	Glu	Phe	Leu	Gln	Arg	Asp	Phe	Ser	Glu	Thr	Tyr	Glu		
			260					265					270				
Arg	Tyr	His	Thr	Glu	Ser	Leu	Gln	Asn	Met	Ser	Lys	Gln	Glu	Leu	Ile		
		275					280					285					
Lys	Glu	Tyr	Leu	Glu	Leu	Glu	Lys	Cys	Leu	Ser	Arg	Met	Glu	Asp	Glu		
	290					295					300						
Asn	Asn	Arg	Leu	Arg	Leu	Glu	Ser	Lys	Arg	Leu	Gly	Gly	Asp	Asp	Ala		
305					310					315					320		

Arg Val Arg Glu Leu Glu Leu Glu Leu Asp Arg Leu Arg Ala Glu Asn
325 330 335

Leu Gln Leu Leu Thr Glu Asn Glu Leu His Arg Gln Gln Glu Arg Ala
340 345 350

Pro Leu Ser Lys Phe Gly Asp
355

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCTAGGCCG CGAGCTTAGT CCTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA	60
TCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAAT GAAATTCCTT ATCTTCGCAT	120
TTTTCGGTGG TGTTACCTT TTATCCCTGT GCTCTGGGAA AGCTATATGC AAGAATGGCA	180
TCTCTAAGAG GACTTTTGAA GAAATAAAAG AAGAAATAGC CAGCTGTGGA GATGTTGCTA	240
AAGCAATCAT CAACCTAGCT GTTTATGGTA AAGCCCAGAA CAGATCCTAT GAGCGATTGG	300
CACTTCTGGT TGATACTGTT GGACCCAGAC TGAGTGGCTC CAAGAACCTA GAAAAAGCCA	360
TCCAAATTAT GTACCAAAAC CTGCAGCAAG ATGGGCTGGA GAAAGTTCAC CTGGAGCCAG	420
TGAGAATACC CCACTGGGAG AGGGGAGAAG AATCAGCTGT GATGCTGGAG CCAAGAATTC	480
ATAAGATAGC CATCCTGGGT CTTGGCAGCA GCATTGGGAC TCCTCCAGAA GGCATTACAG	540
CAGAAGTTCT GGTGGTGACC TCTTTGATG AACTGCAGAG AAGGGCCTCA GAAGCAAGAG	600
GGAAGATTGT TGTTTATAAC CAACCTTACA TCAACTACTC AAGGACGGTG CAATACCGAA	660
CGCAGGGGGC GGTGGAAGCT GCCAAGGTGG GGGCTTTGGC ATCTCTCATT CGATCCGTGG	720
CCTCCTTCTC CATCTACAGT CCTCACACAG GTATTCAGGA ATACCAGGAT GGCGTGCCCA	780
AAATTCCAAC AGCCTGTATT ACGGTGGAAG ATGCAGAAAT GATGTCAAGA ATGGCTTCTC	840
ATGGGATCAA AATTGTCATT CAGCTAAAGA TGGGGGCAAA GACCTACCCA GATACTGATT	900
CCTTCAACAC TGTAGCAGAG ATCACTGGGA GCAAATATCC AGAACAGGTT GTACTGGTCA	960
GTGGACATCT GGACAGCTGG GATGTTGGGC AGGGTGCCAT GGATGATGGC GGTGGAGCCT	1020
TTATATCATG GGAAGCACTC TCACTTATTA AAGATCTTGG GCTGCGTCCA AAGAGGACTC	1080

TGCGGCTGGT GCTCTGGACT GCAGAAGAAC AAGGTGGAGT TGGTGCCTTC CAGTATTATC	1140
AGTTACACAA GGTAATATT TCCAACCTACA GTCTGGTGAT GGAGTCTGAC GCAGGAACCT	1200
TCTTACCCAC TGGGCTGCAA TTTACTGGCA GTGAAAAGGC CAGGGCCATC ATGGAGGAGG	1260
TTATGAGCCT GCTGCAGCCC CTCAATATCA CTCAGGTCCT GAGCCATGGA GAAGGGACAG	1320
ACATCAACTT TTGGATCCAA GCTGGAGTGC CTGGAGCCAG TCTACTTGAT GACTTATACA	1380
AGTATTTCTT CTTCCATCAC TCCCACGGAG ACACCATGAC TGTCATGGAT CCAAAGCAGA	1440
TGAATGTTGC TGCTGCTGTT TGGGCTGTTG TTTCTTATGT TGTTGCAGAC ATGGAAGAAA	1500
TGCTGCCTAG GTCCTAGAAA CAGTAAGAAA GAAACGTTTT CATGCTTCTG GCCAGGAATC	1560
CTGGGTCTGC AACTTTGGAA AACTCCTCTT CACATAACAA TTTCATCCAA TTCATCTTCA	1620
AAGCACAACCT CTATTTTCATG CTTTCTGTTA TTATCTTTCT TGATACTTTC CAAATTCCTCT	1680
GATTCTAGAA AAAGGAATCA TTCTCCCCTC CCTCCCACCA CATAGAATCA ACATATGGTA	1740
GGGATTACAG TGGGGGCATT TCTTTATATC ACCTCTTAAA AACATTGTTT CCACTTTAAA	1800
AGTAAACACT TAATAAATTT TTGGAAGATC TCTGAAAAAA AAAAAAAAAA A	1851

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Lys	Phe	Leu	Ile	Phe	Ala	Phe	Phe	Gly	Gly	Val	His	Leu	Leu	Ser
1				5					10					15	
Leu	Cys	Ser	Gly	Lys	Ala	Ile	Cys	Lys	Asn	Gly	Ile	Ser	Lys	Arg	Thr
			20					25					30		
Phe	Glu	Glu	Ile	Lys	Glu	Glu	Ile	Ala	Ser	Cys	Gly	Asp	Val	Ala	Lys
			35				40					45			
Ala	Ile	Ile	Asn	Leu	Ala	Val	Tyr	Gly	Lys	Ala	Gln	Asn	Arg	Ser	Tyr
			50			55					60				
Glu	Arg	Leu	Ala	Leu	Leu	Val	Asp	Thr	Val	Gly	Pro	Arg	Leu	Ser	Gly
65				70					75					80	
Ser	Lys	Asn	Leu	Glu	Lys	Ala	Ile	Gln	Ile	Met	Tyr	Gln	Asn	Leu	Gln
			85					90						95	

Gln	Asp	Gly	Leu	Glu	Lys	Val	His	Leu	Glu	Pro	Val	Arg	Ile	Pro	His			
			100					105					110					
Trp	Glu	Arg	Gly	Glu	Glu	Ser	Ala	Val	Met	Leu	Glu	Pro	Arg	Ile	His			
			115				120						125					
Lys	Ile	Ala	Ile	Leu	Gly	Leu	Gly	Ser	Ser	Ile	Gly	Thr	Pro	Pro	Glu			
			130			135					140							
Gly	Ile	Thr	Ala	Glu	Val	Leu	Val	Val	Thr	Ser	Phe	Asp	Glu	Leu	Gln			
145					150					155					160			
Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly	Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro			
				165					170					175				
Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val	Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val			
			180					185					190					
Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu	Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala			
			195				200					205						
Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His	Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp			
			210			215					220							
Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala	Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu			
225					230					235					240			
Met	Met	Ser	Arg	Met	Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu			
				245					250					255				
Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val			
			260					265					270					
Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser			
			275				280						285					
Gly	His	Leu	Asp	Ser	Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly			
			290			295					300							
Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu			
305					310					315					320			
Gly	Leu	Arg	Pro	Lys	Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu			
				325					330					335				
Glu	Gln	Gly	Gly	Val	Gly	Ala	Phe	Gln	Tyr	Tyr	Gln	Leu	His	Lys	Val			
			340					345					350					
Asn	Ile	Ser	Asn	Tyr	Ser	Leu	Val	Met	Glu	Ser	Asp	Ala	Gly	Thr	Phe			
			355				360					365						
Leu	Pro	Thr	Gly	Leu	Gln	Phe	Thr	Gly	Ser	Glu	Lys	Ala	Arg	Ala	Ile			
			370			375					380							
Met	Glu	Glu	Val	Met	Ser	Leu	Leu	Gln	Pro	Leu	Asn	Ile	Thr	Gln	Val			
385					390					395					400			
Leu	Ser	His	Gly	Glu	Gly	Thr	Asp	Ile	Asn	Phe	Trp	Ile	Gln	Ala	Gly			

405	410	415
Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe		
420	425	430
His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met		
435	440	445
Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp		
450	455	460
Met Glu Glu Met Leu Pro Arg Ser		
465	470	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGAAGTTCA AGGGCCCCCG GCCTCCTGCG CTCCTGCCGC CGGGACCCTC GACCTCCTCA	60
GAGCAGCCGG CTGCCGCCCC GGAAGATGG CGAGGAGGAG CCGCCACCGC CTCCTCCTGC	120
TGCTGCTGCG CTACCTGGTG GTCGCCCTGG GCTATCATAA GGCCTATGGG TTTTCTGCCC	180
CAAAAGACCA ACAAGTAGTC ACAGCAGTAG AGTACCAAGA GGCTATTTTA GCCTGCAAAA	240
CCCCAAAGAA GACTGTTTCC TCCAGATTAG AGTGGAAGAA ACTGGGTCGG AGTGTCTCCT	300
TTGTCTACTA TCAACAGACT CTTCAAGGTG ATTTTAAAAA TCGAGCTGAG ATGATAGATT	360
TCAATATCCG GATCAAAAAT GTGACAAGAA GTGATGCGGG GAAATATCGT TGTGAAGTTA	420
GTGCCCCATC TGAGCAAGGC CAAAACCTGG AAGAGGATAC AGTCACTCTG GAAGTATTAG	480
TGGCTCCAGC AGTTCCATCA TGTGAAGTAC CCTCTTCTGC TCTGAGTGGA ACTGTGGTAG	540
AGCTACGATG TCAAGACAAA GAAGGGAATC CAGCTCCTGA ATACACATGG TTTAAGGATG	600
GCATCCGTTT GCTAGAAAAT CCCAGACTTG GCTCCCCAAG CACCAACAGC TCATACACAA	660
TGAATACAAA AACTGGAAC TCGCAATTTA ATACTGTTTC CAAACTGGAC ACTGGAGAAT	720
ATTCCTGTGA AGCCCGCAAT TCTGTTGGAT ATCGCAGGTG TCCTGGGAAA CGAATGCAAG	780
TAGATGATCT CAACATAAGT GGCATCATAG CAGCCGTAGT AGTTGTGGCC TTAGTGATTT	840
CCGTTTGTGG CCTTGGTGTA TGCTATGCTC AGAGGAAAGG CTACTTTTCA AAAGAAACCT	900

CCTTCCAGAA GAGTAATTCT TCATCTAAAG CCACGACAAT GAGTGAAAAT GATTTC AAGC 960
ACACAAAATC CTTTATAATT TAAAGACTCC ACTTTAGAGA TACACCAAAG CCACCGTTGT 1020
TACACAAGTT ATTAAACTAT TATAAAACTC AAAAAAAAAA AAAAAAAAAA AAAAAA 1076

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Tyr	1	5	10	15
Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser	Ala	Pro	20	25	30	
Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu	35	40	45	
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys	50	55	60	
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln	65	70	75	80
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile	85	90	95	
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser	100	105	110	
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu	115	120	125	
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser	130	135	140	
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly	145	150	155	160
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu	165	170	175	
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met	180	185	190	
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp				

195	200	205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg		
210	215	220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
225	230	235
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
245	250	255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
260	265	270
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
275	280	285
Asp Phe Lys His Thr Lys Ser Phe Ile Ile		
290	295	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAAGGTTGT GTAGCTTGCC CTGGTTGCAT AGTTAAACGA GGGCTAGAAA CAGGACTAGG	60
AGTCAGGCCT GTCCAGCTGG AAAACTTGGG TTTTCTAGAA GGGGTACCCT GGCCTCCTGC	120
GGAGCCTGCT GTGGGACTCT GCAGAACACA ATTCAAGGCC AGACTGAACA CTAGCCTGAA	180
CCTGCCCTGA GAATCCCTCT AAGCCGACCT ACTCCACAGC TGTCCTGACT GTGTAAGCGA	240
GATGATGATT AGTGATCAGA CGAAAGGATT CCTGTCATTG GTAACCCTCT CAAAGTATTT	300
GGAAAACAGT TCAATTTTCA TCTATTTTCA AAGCACGCCG TGGTGTCTAT TGAGGCTCAC	360
CTGCATTGAA TTCCTTCCTT TTTATGTTGC GATCTCCCAA GATTGCATTG TGGAGTGTTT	420
TCGAATCCAT TTTGAAATCC CCGTGCGTGC GCTATGCAGG CCTCAGTCTT TTTCCATTCC	480
ATTCTTAACT CTACTTTCGA CGGAAGCAGT GTTTTACCCC GAACTGGCT TGCCTAGGAC	540
CTTGCTCTCT GCACAACTAG CAGGGCCCGG CAGGATGTAC TGAATTCTTG CTCTCGTGTC	600
CAGCTGGACG GTGATGGCTT TCAAGTCCTT GGCTGTTGGG AGCTTACTAT AAATGTTTCGT	660
CTTGGCTACA AACTCTCCAC TCTTTCCTCG GCACTCTCTC AGCATTGCCA CCACTGTCTT	720

TCCTCTTGGC	CAACTGTTTT	CTTTACTTAG	GCTTTCCCTT	GCTAGAAAGT	CCAGGTAACT	780
TTCTCCACGG	GACCTGGTTT	CCTTCGCACA	TCCCAGCTGG	CCTCGAGGAA	AGGTAGCTCT	840
TCCAAATCAG	AGAATCTGGA	TGCTGGGCTG	GGCTCTGCAC	CAACCAGCTG	GGCCGCTTCA	900
CCCCTGGGGC	CCCAAACACTAC	TCATCTGTGA	AGCGAAGGCA	CCGCGCTTGA	TGCCTTCTGC	960
AACGTTCTTC	AGTTTGGAAA	TCCTTCTGTT	TCGTTGGGGA	TATTTACAGG	CCTCTTCTCA	1020
AGGTTGCACT	TTTGCCAGCT	GCCAGGGATC	GTCTCAAAAC	AGGTTCTTAG	TGCATTCTATA	1080
GCTTGAGCTG	CTGTCTTGAA	AGTAGTACAT	TCCTTTTTCT	GCCAACTTTT	TTCTGAGAAA	1140
GTTTTTGAAT	GCACACGTGC	ACCCAACAGA	GTGAGAGTGG	CTGTAAAGAG	AGAGGGCGCC	1200
ATTTCTTTTG	CCCTCCAGCC	TGTCCCTGTG	CACCCTGGAG	GGGCCCCTTT	TTTCCACCGC	1260
TTAGATAAAA	TCTAGGGCAA	GTTCTGAAC	TTCTCTTGTC	TCTCTCAGGT	AACAAAAATT	1320
CTTTTGGGCT	CCTTTAGTCA	CAAAGATATT	CACGATTTCA	GGTATTAAAG	TGCCCAGCCC	1380
TGGGTGATTG	TCAAAATTCT	GAAGTTGATT	TAAAGTGGCA	CCTCCTCTCA	CAGTCTTCGG	1440
GAGGGAGAGA	CCGGAGCCAG	GAGTGCAGCG	TGTTTGCTGG	GGTCTGTCGT	GGCCCACTCC	1500
ACACCTGCTG	GGTGGATCCG	GCTGGTGCCC	CATGGGCGCC	TCTGAGATGC	CCCTCCCCAC	1560
CCCATCAGTG	GCGCTGTCTC	ACCTGCAGGC	TGTTCTCACA	GGTGGTCCCC	CCTCACTCCT	1620
CCTGCAGCCC	CAGTTCTTGG	CTGTTTATTC	TTATTGGGAC	CCGTCACCCT	CCTGGAGGCG	1680
GTCCCAGCCG	AGCCCCCTTA	AGACAGCACC	AGGCTGGCTC	CACTTGGCCC	CCGCTGGTTC	1740
AGGGAAGTGC	TGCTGCAGCC	GTTTAGTTTG	ACAAAGGAGG	CAGCGAGGCC	GTCTCATTGG	1800
TAGCCCTCTC	CTGGCTTGCC	CAGCCACCAC	CTCACCTCGA	TTCCTCCCAG	GCCTGGGTCC	1860
AGCACCAGCC	TAGGAAGAGG	GTGCCCCATG	CTGTCTAGCT	CTTCTTCGGG	ATGGGGGGCT	1920
CCAGGTTCTT	TGGTATTTTG	CTTTGGCCTT	TGGAGCCTCA	GTCAAACTG	AGGAAAGGTG	1980
TCATTTTCAC	ATCTCGTCAC	ACGTACAGTG	ACTGCAACTA	AAAGCACAGG	CTTTGTAGAA	2040
ACAGACATGG	GTTTACAGCCC	CAGCTCCACC	ATTACACAAGG	TGTGTGGCTT	CCTGCAAGGT	2100
ACCTTCATCT	CTGAGTTACC	TGACTCCATC	TGAGTTTCCT	TCTTGTAATA	CTGGCATCCA	2160
TGAAAGTGGC	TACCTCGAAG	GGCGTGAAGA	TGAAATGAGG	TGGAAAGTAG	GTAGCCCCCG	2220
AATGAGGGAA	GCATTGAGTG	AGAGCTGGCC	CTCTGACCCT	TCTAAAAGAA	CACAGCCAAC	2280
TTTTTAAACT	GTCTTTCCAG	AAAGAGATGG	AAAACCTCGA	AGCCCCCTTC	CACTGCCTTG	2340
CCAAGCAGTT	CCACCAGCTG	TACCGGGAGA	AGGTGGAGGT	TTTCCGGGCC	CTGGCATGAC	2400
GAGCTGGAGC	AGATCGTGCT	GCACAACCGG	AGAAGACAGA	ATTACCTCTG	CTCTTTTAAT	2460

ATATAATGAT GGCTTTAAAT AAAATTAGGA GAAAATGTCA AAAAAAAAAA AAAAAAAAAA 2520

AA 2522

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Met Ile Ser Asp Gln Thr Lys Gly Phe Leu Ser Leu Val Thr Leu
1 5 10 15
Ser Lys Tyr Leu Glu Asn Ser Ser Ile Phe Ile Tyr Phe Arg Ser Thr
20 25 30
Pro Trp Cys Leu Leu Arg Leu Thr Cys Ile Glu Phe Leu Pro Phe Tyr
35 40 45
Val Ala Ile Ser Gln Asp Cys Ile Val Glu Cys Phe Arg Ile His Phe
50 55 60
Glu Ile Pro Val Arg Ala Leu Cys Arg Pro Gln Ser Phe Ser Ile Pro
65 70 75 80
Phe Leu Thr Leu Leu Ser Thr Glu Ala Val Phe Tyr Pro Asp Thr Gly
85 90 95
Leu Pro Arg Thr Leu Cys Ser Ala Gln Leu Ala Gly Pro Gly Arg Met
100 105 110
Tyr

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGGGCCCC AGCCTTCTCC AGAACCCCTG CTACCCACGA CTAAGCCCCG AACAATCTGC 60
CCTTGGGCTT GTTCTCTTCG CAGTTGTCGG CCCTGGGCCG GGAGCTGGAG TCCCAGACTC 120

ATAGGTCCCG	CCCCAGCCCC	CGAAGAGCCG	CCTCAGCCGG	GGGGAGTTGC	TCGGACTCAA	180
ACGTCCAGTC	CTCGTGCGAC	CGCGCTGGGT	CGGAAGTGAG	CAGGCTGAGG	CCACCATGGA	240
GCAGTGTGCG	TGCGTGAGGA	GAGAGCTGGA	CAAGGTCTCG	CAGAAGTTCC	TGACCTACGG	300
GCAGCACTGT	GAGCGGAGCC	TGGAGGAGCT	GCTGCACTAC	GTGGGCCAGC	TGCGGGCTGA	360
GCTGGCCAGC	GCAGCCCTCC	ARGGGACCCC	TCTCTCAGCC	ACCCTCTCTC	TGGTGATGTC	420
ACAGTGCTGC	CGGAAGATCA	AAGATACGGT	GCAGAACTG	GCTTCGGAMC	ATAAGGACAT	480
TCACAGCAGT	GTATCCCGAG	TGGGCAAAGC	CATTGACAGG	AACTTCGACT	CTGAGATCTG	540
TGGTGTTGTG	TCAGATGCGG	TGTGGGACGC	GCGGGAACAG	CAGCAGCAGA	TCCTGCAGAT	600
GGCCATCGTG	GAACACCTGT	ATCAGCAGGG	CATGCTCAGC	GTGGCCGAGG	AGCTGTGCCA	660
GGAATCAACG	CTGAATGTGG	ACTTGGATTT	CAAGCAGCCT	TTCCTAGAGT	TGAATCGAAT	720
CCTGGAAGCC	CTGCACGAAC	AAGACCTGGG	TCCTGCGTTG	GAATGGGCCG	TCTCCACAG	780
GCAGCGCCTG	CTGGAActCA	ACAGCTCCCT	GGAGTTCAAG	CTGCACCGAC	TGCACTTCAT	840
CCGCCTCTTG	GCAGGAGGCC	CCGCGAAGCA	GCTGGAGGCC	CTCAGCTATG	CTCGGCACTT	900
CCAGCCCTTT	GCTCGGCTGC	ACCAGCGGGA	GATCCAGGTG	ATGATGGGCA	GCCTGGTGTA	960
CCTGCGGCTG	GGCTTGAGGA	AGTCACCCTA	CTGCCACCTG	CTGGACAGCA	GCCACTGGGC	1020
AGAGATCTGT	GAGACCTTTA	CCCGGGACGC	CTGTTCCCTG	CTGGGGCTTT	CTGTGGAGTC	1080
CCCCCTTAGC	GTCAGCTTTG	CCTYTGGCTG	TGTGGCGCTG	CCTGTGTTGA	TGAACATCAA	1140
GGCTGTGATT	GAGCAGCGGC	AGTGCACCTG	GGTCTGGAAT	CACAAGGACG	AGTTACCGAT	1200
GAGATTGAAC	TAGGCATGAA	GTGCTGGTAC	CACTCCGTGT	TCGCTTGCCC	CATCCTCCGC	1260
CAGCAGACGT	CAGATTCCAA	CCCTCCCATC	AAGCTCATCT	GTGGCCATGT	TATCTCCCGA	1320
GATGCACTCA	ATAAGCTCAT	TAATGGAGGA	AAGCTGAAGT	GTCCCTACTG	TCCCATGGAG	1380
CAGAACCCGG	CAGATGGGAA	ACGCATCATA	TTCTGATTCC	TACCTGGAAG	GAATTTTGTT	1440
GAAAGGGGTT	TTCACCTGTG	AGCCTTGGTC	TGTCTCGGTA	GGGTGGTCAA	CTTCAGTGGA	1500
CTGTGGTTGG	TTTCAGAGCG	CCTGGCTGAG	GAGTTCCACT	GAGGGGAGCA	CTGGAGCAGC	1560
CCTTTGGCAG	AGGCTGAGGA	GGGAGATGGA	CCAGCCCACG	CCTGGCACCT	GGCTCCATGG	1620
CATAAGGAAA	GGGAGATGCT	GGCCTCTGTG	CTCCTGCTGT	CTTTTCCTGT	TTCTGTTTGC	1680
GTTTGAActTA	GTagCAACCG	ACAGAGTGGC	AAGGGATTTG	GTCTTCAGCA	GTagACATCC	1740
TTCCACCCCT	GCCCTCAGCC	AAGTCTCTTG	CTGCCATGCC	AATGCTATGT	CCACCCCTTG	1800

CCCTCGGCCC AAGAGTGTCC AGCGGTGGCC CACYTYTTCC TCCCACTACA GCCTCAACAG 1860
TATGTACCAT CTCCCACTGT AAATAGTCCC AGTTAGAACG GAATGCCGTT GTTTTATAAC 1920
TTTGAACAAA TGTATTTACT GCCAAAAAAA AAAAAAAAAA AA 1962

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Glu	Gln	Cys	Ala	Cys	Val	Glu	Arg	Glu	Leu	Asp	Lys	Val	Leu	Gln	1	5	10	15
Lys	Phe	Leu	Thr	Tyr	Gly	Gln	His	Cys	Glu	Arg	Ser	Leu	Glu	Glu	Leu	20	25	30	
Leu	His	Tyr	Val	Gly	Gln	Leu	Arg	Ala	Glu	Leu	Ala	Ser	Ala	Ala	Leu	35	40	45	
Gln	Gly	Thr	Pro	Leu	Ser	Ala	Thr	Leu	Ser	Leu	Val	Met	Ser	Gln	Cys	50	55	60	
Cys	Arg	Lys	Ile	Lys	Asp	Thr	Val	Gln	Lys	Leu	Ala	Ser	Xaa	His	Lys	65	70	75	80
Asp	Ile	His	Ser	Ser	Val	Ser	Arg	Val	Gly	Lys	Ala	Ile	Asp	Arg	Asn	85	90	95	
Phe	Asp	Ser	Glu	Ile	Cys	Gly	Val	Val	Ser	Asp	Ala	Val	Trp	Asp	Ala	100	105	110	
Arg	Glu	Gln	Gln	Gln	Gln	Ile	Leu	Gln	Met	Ala	Ile	Val	Glu	His	Leu	115	120	125	
Tyr	Gln	Gln	Gly	Met	Leu	Ser	Val	Ala	Glu	Glu	Leu	Cys	Gln	Glu	Ser	130	135	140	
Thr	Leu	Asn	Val	Asp	Leu	Asp	Phe	Lys	Gln	Pro	Phe	Leu	Glu	Leu	Asn	145	150	155	160
Arg	Ile	Leu	Glu	Ala	Leu	His	Glu	Gln	Asp	Leu	Gly	Pro	Ala	Leu	Glu	165	170	175	
Trp	Ala	Val	Ser	His	Arg	Gln	Arg	Leu	Leu	Glu	Leu	Asn	Ser	Ser	Leu	180	185	190	
Glu	Phe	Lys	Leu	His	Arg	Leu	His	Phe	Ile	Arg	Leu	Leu	Ala	Gly	Gly	195	200	205	

Pro Ala Lys Gln Leu Glu Ala Leu Ser Tyr Ala Arg His Phe Gln Pro
 210 215 220
 Phe Ala Arg Leu His Gln Arg Glu Ile Gln Val Met Met Gly Ser Leu
 225 230 235 240
 Val Tyr Leu Arg Leu Gly Leu Glu Lys Ser Pro Tyr Cys His Leu Leu
 245 250 255
 Asp Ser Ser His Trp Ala Glu Ile Cys Glu Thr Phe Thr Arg Asp Ala
 260 265 270
 Cys Ser Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 275 280 285
 Ala Xaa Gly Cys Val Ala Leu Pro Val Leu Met Asn Ile Lys Ala Val
 290 295 300
 Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn His Lys Asp Glu Leu
 305 310 315 320
 Pro Met Arg Leu Asn
 325

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAAAACACAA AACCCCGTAA AATCACAAAG AAAATCCAAC ACCAAAGGCG CAGAAGCCGG 60
 CTGGCCGTGG TGGGGGCAGC GTAGGCGTAG CATCCCTCTC CTCTCACTTA GCCTGTTGAC 120
 TCTTGTTATT ATCATGATAT TCACAAAACG CCGCATGTTT AAAAAGTCAT AGATGTCATC 180
 TTCTCTCTGC CCCAGGGAG GAAAGCCACC TTCTCTTGCC CCTTGGCCCC TTTGTCAGGG 240
 GCCAGGGGTC TGCCGGGTGG GGGTGCCAAC AGGCCTGGCC CTTTCCTCCC CTGCATCCAG 300
 CCATGGGGGC CTCTGCGATT GCCGGAAGGT TGCATGGCTG GTCCCAGGGC CAGCACAGGC 360
 CCGAGGCCGG GCTGCCTGGT TTTATTTTTA TTAACTTTA TTTTCTGTTT TATGAGTGTG 420
 TGTCCGCCCA CCCCCACCCC CTTCA GTGTT AAGTGGGGAG CCCTGGGGGA GTCTCTCCTG 480
 CCTCCCAGCC TCTCCAAGA CCTCCCCCT CGTCACCAGC CATCCCTCTG GACCAGGCAG 540

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AGGGCGGACC GGGTGGGCAG GGGCCTGAGG GTGGCTCGGG CCAGCCCACC AGCCAATGGA      600
CCCCTCCTCA GGCCGCCAGT GTCGCCCTGC CCCTTTTTTAA AACAAAATGC CCTCGTTTGT      660
AAACCCTTAG ACGCTTGAGA ATAAACCCCT TCCTTTTCTT CCAAAAAAAAAA AAAAAAAAAA      720
AAAAAAAAAA AAAAAAAAAA AAAAAA                                         745

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(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Ala Gly Pro Arg Ala Ser Thr Gly Pro Arg Pro Gly Cys Leu Val
 1              5              10              15

Leu Phe Leu Phe Asn Phe Ile Phe Cys Phe Met Ser Val Cys Pro Pro
      20              25              30

Thr Pro Thr Pro Phe Ser Val Lys Trp Gly Ala Leu Gly Glu Ser Leu
 35              40              45

Leu Pro Pro Ser Leu Ser Gln Asp Leu Pro Pro Arg His Gln Pro Ser
 50              55              60

Leu Trp Thr Arg Gln Arg Ala Asp Arg Val Gly Arg Gly Leu Arg Val
 65              70              75              80

Ala Arg Ala Ser Pro Pro Ala Asn Gly Pro Leu Leu Arg Pro Pro Val
      85              90              95

Ser Pro Cys Pro Phe Leu Lys Gln Asn Ala Leu Val Cys Lys Pro Leu
      100             105             110

Asp Ala

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1983 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGGCAATAGT GGTTAGGGAA GGCTCCTTTG AGGAAGTGAA TTTT TAGCTG AGACTTAAAG 60
AACAAATGAG ATTTAGCTAG AAAAATTGGA CATGCGATGC CAAGATGGCA TTTTAAAAGA 120
ATAATAGTAA GCACAAAGGC CCTGTAGCAG GAGGGAGCTG ATTGTCCATA GTTCAGACAG 180
CAAAGAAGCT GATGATGCAG GTTGGGGTCA GACCGTGTTT GACTACAGAT AGGATGTTAA 240
GGGTTTGGC TTTT TAGGTT TTTGTTTAA TTCTAAAAGT AATGGAAAAT GTACTCCTTT 300
TGGTGGTGGT CTGAGAGAAG GTACATCATT AGAATGACAT TTTGAAAACA AACTCAGGC 360
TGCTCAGTAG AGAATGGCTT CAAAGGATTT AAAAGCAGAA GCAGAAGGAC ATATTAGAGA 420
AGGATTGTAT AGTTTCTGG TAAAAGATGA CAGTGAATTG TATGGGCGAT GGATTAGCCG 480
TGGAAGGTGT TGAGTATAAG TGGTCTCCAG CCAA CTCTA TGGTTACTGG AATAAGAGAG 540
TAGGAACCTT TCTCAGGCTT TATCTTTATC TATTCTTGTC AACAGTATGT ACATGTGTCC 600
CCCAGCCCCA AATACTGTA CAGTTTAATG ATGTTCACTC TATACAGTTC CCAGAATCCA 660
TTGGAAATTG CTGTAACAGC ATATCCTCAA TGCCCATCAA TTCTCCACGT CCAACTTCTC 720
CATGGCCTCC TCTGCCTCTG CTGATCTGTG AACTTCCCAA GCCCCTTCCC CTACCTGCTT 780
TTGATTGGCT TTAAC TTTTA CAATATCTTC ATTACTCAA GTTTGTTCAA CATCCTTTTT 840
ATTTTTTTAA ATCATAGATT GATTTAGTTT ATTCTCTTTG CCATTTTTGA ATCTCATTAT 900
TTCTGTTTCT CCTTGGTTAT TAGTGGCTCT GTTTTCCTTC AATTGCCTCT TGTCTTTGAG 960
AAGCTCTTGT GATTCTTTTA GGGCCATTTG CCATTGATT GGTGTGTCTT CCTTTCCCT 1020
ATAAGCTTTA AATATGGCAT TATAGTTTTA TCCCCTTTCC TCTTCTTTAG GTACAACTGC 1080
AGACACTTTG CTCTCCAAG GTTACTAAGC AGTGTCTGAC ACAATGTAGA AGCTCAACAA 1140
ATATTGGTTA AATTATTTT TCTATTGAT TGTTCAGGCT TTGATGACAT CACTTAAAT 1200
GTTTCTTGTA CACACCCTGT TTTCTACTGA TATATGTATG TGTATGGCTA CCTGAATCCA 1260
GGTTTCTTCT AGGAATATAC AGAAAGTAAT TGATTCTCT GTGGATCTCT AACAGTGACA 1320
AGAATTTTCA CCTATGCCTG TGAGAATACC TTCAAAAGTA TTGGGTGCTC ATCATAAACA 1380
CACATCAGTT TAACAACTC TTATGGATGC ATTGACTTTC CCAGTTAGTT GCTAGATGAC 1440
TTCGGATGAT TTGCATAATG GGTCTCAGTT TCCATATCTG TTAAATGGCA ATAATCAGAG 1500
AATTTTAAAA AATTTAAGGA CACCTGGAAA GCTTGAAAGA TCCCTAGAAA GCATGTGTTT 1560
ATTCCACATA GTGGGAACTA TGCTAGATTC CCAAAGACAC AAAGACAACT AAGACAACTT 1620

AGAATAAGAA GGAAAAGAGA ATGATTCGTT GCAATGATCC CCTTGAAGCT CCAGTTGAAA 1680
 GTCAGAGTAT TGCCCTGGAT TGGAAGTAGT CTCCAAACTG ACATCATTTT CTTTTTCGAA 1740
 CCATATCTGG CCTGTCTCTC TTGCCAGTTG CATATTAAAG GTAACAGATT TGAAAATGTT 1800
 TGGAATAAAA GCTCTAGTTA GGTGTGGTGG CACACACCTG CCATCCCAGC TACTGGAGAG 1860
 TCTGAGACTC GATGATTGTT TCAGCCCAAG AGTTGGAGGT TGTAGTGAGC TATGATGGCA 1920
 CCACTGCACT CCAGTCTGTG TGACAGAGCG AAGACCTTGT CTCTAAGGAA AAAAAAAAAA 1980
 AAA 1983

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Thr Val Asn Cys Met Gly Asp Gly Leu Ala Val Glu Gly Val Glu
 1 5 10 15
 Tyr Lys Trp Ser Pro Ala Lys Leu Tyr Gly Tyr Trp Asn Lys Arg Val
 20 25 30
 Gly Thr Leu Leu Arg Leu Tyr Leu Tyr Leu Phe Leu Ser Thr Val Cys
 35 40 45
 Thr Cys Val Pro Gln Pro Gln Ile Thr Val Gln Phe Asn Asp Val His
 50 55 60
 Ser Ile Gln Phe Pro Glu Ser Ile Gly Asn Cys Cys Asn Ser Ile Ser
 65 70 75 80
 Ser Met Pro Ile Asn Ser Pro Arg Pro Thr Ser Pro Trp Pro Pro Leu
 85 90 95
 Pro Leu Leu Ile Cys Glu Leu Pro Lys Pro Leu Pro Leu Pro Ala Phe
 100 105 110
 Asp Trp Leu
 115

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1046 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGCTTAGTT AGGAGCTATG GCTAAACATC ATCCTGATTT GATCTTTTGC CGCAAGCAGG	60
CTGGTGTGTC CATCGGAAGA CTGTGTGAAA AATGTGATGG CAAGTGTGTG ATTTGTGACT	120
CCTATGTGCG TCCCTGCACT CTGGTGCGCA TATGTGATGA GTGTAACTAT GGATCTTACC	180
AGGGGCGCTG TGTGATCTGT GGAGGACCTG GGGTCTCTGA TGCCTATTAT TGTAAGGAGT	240
GCACCATCCA GGAGAAGGAC AGAGATGGCT GCCCAAAGAT TGTC AATCTG GGGAGCTCTA	300
AGACAGACCT CTTCTATGAA CGCAAAAAAT ACGGCTTCAA GAAGARGTGA TTGGTGGGTG	360
GCCCCCTCCT CCCCCCAACA TCAGTCTGCT GCAGCTGCCA GAAAACATGC CTACTACTAC	420
CAGCAGAAAG GGAGCAGAGC CCAGAGCATC ACCAGGAGTG CCTGCTAGTG TACTGGCAGC	480
TTGCCACCCC CTCCTCTCCC TTCACCCAGA CACGTGGTAG GGATGGAAAA GGATTCTTCA	540
CAGAGCACTC TGGCACACCA TATCGGAGAA AACTTGATAG ATTAGTTAAT GGTTTTTCTT	600
GAATTCGAGA AGCATAGATC TGTTCTCCAT ATTGGTATGT TCTCCCTCAA CCAAGATCTT	660
CTAAAAAGAA ATAATATTTT AGTCTTCTGC TTGAGGAACT GACTGTGAAG CGACGCCCAG	720
TGAAAAACAT GTTCTTGCA GAGCTCTGGT GGCAGCTGTC CTTGAGGAAC CTTTGGTGTG	780
TGGTGGGAAG CTATCAGAAC AAGAAATGTA GGCATTTCCC GTTTTTTTGG GGGGGGGGGG	840
TGGGGGGGCA GGGCTCTGCC CTCTTGAAAG GCATTTACTT GTTTAACTACT TGTCCAGCTA	900
CAGTGGGGTA CAGTAGCTGG CTATTCACAG GCATCATCAT AGCCCACTAG TCTCATATTA	960
TTTTCCTTTT GAGAAATTGG AACTCTTTC TGTGCTATT ATATTAATAA AGTTGGTGTT	1020
TATTTTCTGG TAAAAAAAAA AAAAAA	1046

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Ala	Lys	His	His	Pro	Asp	Leu	Ile	Phe	Cys	Arg	Lys	Gln	Ala	Gly	
1				5					10					15		
Val	Ala	Ile	Gly	Arg	Leu	Cys	Glu	Lys	Cys	Asp	Gly	Lys	Cys	Val	Ile	
			20					25					30			
Cys	Asp	Ser	Tyr	Val	Arg	Pro	Cys	Thr	Leu	Val	Arg	Ile	Cys	Asp	Glu	
		35					40					45				
Cys	Asn	Tyr	Gly	Ser	Tyr	Gln	Gly	Arg	Cys	Val	Ile	Cys	Gly	Gly	Pro	
	50					55					60					
Gly	Val	Ser	Asp	Ala	Tyr	Tyr	Cys	Lys	Glu	Cys	Thr	Ile	Gln	Glu	Lys	
65					70					75					80	
Asp	Arg	Asp	Gly	Cys	Pro	Lys	Ile	Val	Asn	Leu	Gly	Ser	Ser	Lys	Thr	
				85					90					95		
Asp	Leu	Phe	Tyr	Glu	Arg	Lys	Lys	Tyr	Gly	Phe	Lys	Lys	Xaa			
			100					105					110			

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCTTGCAGT	GGGCCTCTGT	CCCAAAAACA	AGCAGAATTT	TTTCTTTCTC	AACAGGCTTC	60
TTTGCTAAAG	AATGATGAGA	CTAAGGCCCT	CACTCCAGCT	TCCTTGCAGA	AGGAATTAAA	120
CAATTTGTTG	AAATTTAATC	CTGATTTTGC	TGAAGCGCAT	TATCTCAGCT	ACTTAAACAA	180
CCTCCGTGTC	CAAGATGTTT	TCAGTTCAAC	ACACAGTCTC	CTCCATTATT	TTGATCGTCT	240
GATTCTTACC	GGAGCCGAAA	GCAAAAGTAA	TGGGGAAGAR	GGCTATGGCC	GGAGCTTGAG	300
ATACGCCGCT	CTGAATCTTG	CCGCCCTGCA	CTGCCGCTTC	GGTCACTATC	AACAGGCAGA	360
GCTCGCCCTG	CAGGARGCAA	TTAGGATTGC	CCAGGARTCC	AACGATCACG	TGTGTCTCCA	420
GCACTGTTTG	AGCTGGCTTT	ATGTGCTGGG	GCAGAAGAGA	TCCGATAGCT	ATGTTCTGCT	480
GGAGCATTCT	GTGAAGAAGG	CAGTACATTT	TGGGTTACCG	TACCTCGCCT	CCCTGGGAAT	540
ACAGTCCCTT	GTTCAACAGA	GAGCTTTTGC	TGGGAAGACG	GCAAACAAGC	TGATGGATGC	600

CCTAAAGGAC TCCGACYTCC TGCACTGGAA ACACAGCCTG TCAGAGCTCA TCGATATCAG	660
CATCGCACAG AAAACGGCCA TCTGGAGGCT GTATGGCCGC AGCACCATGG CACTGCAACA	720
GGCCCAGATG TTGCTGAGCA TGAACAGCCT GGAGGCGGTG AATGCGGGCG TGCAGCAGAA	780
CAACACAGAG TCCTTTGCTG TCGCACTCTG CCACCTCGCA GAGCTACACG CGGAGCAGGG	840
CTGTTTTGCT GCAGCTTCTG AAGTGTTAAA GCACTTGAAG GAACGATTTT CGCCTAATAG	900
TCAGCACGCC CAGTTATGGA TGCTATGTGA TCAAAAATA CAGTTTGACA GAGCAATGAA	960
TGATGGCAAA TATCATTTGG CTGATTCCT TGTACAGGA ATCACAGCTC TCAATAGCAT	1020
AGAGGGTGTT TATAGGAAAG CGGTTGTATT ACAAGCTCAG AACCAAATGT CAGAGGCACA	1080
TAAGCTTTTA CAAAAATTGT TGGTTCATTG TCAGAACTG AAGAACACAG AAATGGTGAT	1140
CAGTGTCCTA CTGTCCGTGG CAGAGCTGTA CTGGCGATCT TCCTCCCCTA CCATCGCGCT	1200
GCCCATGCTC CTGCAGGCTC TGGCCCTCTC CAAGGAGTAC CGGTTACAGT ACTTGGCCTC	1260
TGAAACAGTG CTGAACTTGG CTTTTGCGCA GCTCATTCTT GGAATCCCAG AACAGGCCTT	1320
AAGTCTTCTC CACATGGCCA TCGAGCCCAT CTTGGCTGAC GGGGCTATCC TGGACAAAGG	1380
TCGTGCCATG TTCTTAGTGG CCAAGTGCCA GGTGGCTTCA GCAGCTTCCT ACGATCAGCC	1440
GAAGAAAGCA GAAGCTCTGG AGGCTGCCAT CGAGAACCTC AATGAAGCCA AGAACTATTT	1500
TGCAAAGGTT GACTGCAAAG AGCGCATCAG GGACGTCGTT TACTTCCAGG CCAGACTCTA	1560
CCATACCCTG GGGAAGACCC AGGAGAGGAA CCGGTGTGCG ATGCTCTTCC GGCAGCTGCA	1620
TCAGGAGCTG CCCTCTCATG GGGTACCCTT GATAAACCAT CTCTAGAGAG GACATCCCTG	1680
CTGGGCTGCT GTGCAGAGTA TAAGATTTTG GACTTGTTCA TGTCCCCTCT CTCCCTATAA	1740
ATGATGTATT TGTGACACCC TATCTTGTC AATAACAGCA TTCTGATTAG TTTGTCTTAA	1800
AAAAAAAAAA AAAA	1814

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Asp Ala Leu Lys Asp Ser Asp Xaa Leu His Trp Lys His Ser Leu

1		5		10		15									
Ser	Glu	Leu	Ile	Asp	Ile	Ser	Ile	Ala	Gln	Lys	Thr	Ala	Ile	Trp	Arg
		20						25					30		
Leu	Tyr	Gly	Arg	Ser	Thr	Met	Ala	Leu	Gln	Gln	Ala	Gln	Met	Leu	Leu
		35					40					45			
Ser	Met	Asn	Ser	Leu	Glu	Ala	Val	Asn	Ala	Gly	Val	Gln	Gln	Asn	Asn
	50					55					60				
Thr	Glu	Ser	Phe	Ala	Val	Ala	Leu	Cys	His	Leu	Ala	Glu	Leu	His	Ala
65					70					75					80
Glu	Gln	Gly	Cys	Phe	Ala	Ala	Ala	Ser	Glu	Val	Leu	Lys	His	Leu	Lys
				85					90					95	
Glu	Arg	Phe	Pro	Pro	Asn	Ser	Gln	His	Ala	Gln	Leu	Trp	Met	Leu	Cys
			100					105					110		
Asp	Gln	Lys	Ile	Gln	Phe	Asp	Arg	Ala	Met	Asn	Asp	Gly	Lys	Tyr	His
		115					120					125			
Leu	Ala	Asp	Ser	Leu	Val	Thr	Gly	Ile	Thr	Ala	Leu	Asn	Ser	Ile	Glu
	130					135					140				
Gly	Val	Tyr	Arg	Lys	Ala	Val	Val	Leu	Gln	Ala	Gln	Asn	Gln	Met	Ser
145					150					155				160	
Glu	Ala	His	Lys	Leu	Leu	Gln	Lys	Leu	Leu	Val	His	Cys	Gln	Lys	Leu
			165						170					175	
Lys	Asn	Thr	Glu	Met	Val	Ile	Ser	Val	Leu	Leu	Ser	Val	Ala	Glu	Leu
			180					185					190		
Tyr	Trp	Arg	Ser	Ser	Ser	Pro	Thr	Ile	Ala	Leu	Pro	Met	Leu	Leu	Gln
		195					200					205			
Ala	Leu	Ala	Leu	Ser	Lys	Glu	Tyr	Arg	Leu	Gln	Tyr	Leu	Ala	Ser	Glu
	210					215					220				
Thr	Val	Leu	Asn	Leu	Ala	Phe	Ala	Gln	Leu	Ile	Leu	Gly	Ile	Pro	Glu
225					230					235				240	
Gln	Ala	Leu	Ser	Leu	Leu	His	Met	Ala	Ile	Glu	Pro	Ile	Leu	Ala	Asp
				245					250					255	
Gly	Ala	Ile	Leu	Asp	Lys	Gly	Arg	Ala	Met	Phe	Leu	Val	Ala	Lys	Cys
		260						265					270		
Gln	Val	Ala	Ser	Ala	Ala	Ser	Tyr	Asp	Gln	Pro	Lys	Lys	Ala	Glu	Ala
		275					280						285		
Leu	Glu	Ala	Ala	Ile	Glu	Asn	Leu	Asn	Glu	Ala	Lys	Asn	Tyr	Phe	Ala
	290					295					300				
Lys	Val	Asp	Cys	Lys	Glu	Arg	Ile	Arg	Asp	Val	Val	Tyr	Phe	Gln	Ala

AAACAACCTG TCCTGTTTTG TCAGTTCCCA GCTTCTTCGT TTAGAATAAA TTAGACCAAA	1020
AGAAGAAACG TGCTTGTCTC TGTATACCCG CAGAATGAAG TTACTGTTGT TAAAACCGGA	1080
TTTTTTCATT TTACTAGGTT CCGAAGAGTC CAGATGCTTG GTAGATGTTC AATACGTGAT	1140
TTTTTTTTTA ATTGAATGTG TTCATTTAAA ATCCTCCTTA ACATTTCTAG AAAGACTTCT	1200
TTCAATAAAT AATGGAATCT TAGAGGAAAA GTGGTTTTTT AAAAGCTAGG GAACTCCTCC	1260
ACTAAAAGTA ACCATTGGAA ACCTCGAATG AGGGCTAAAG TTTTAATCAT AAGAGAAAAG	1320
GCAGCATAAT GAAATGTGTA CACATACATA GTCAGTGGTC CATTTTAGGA AGCCAGTGGC	1380
GTCTGATAAA GAAATGTTAA GAGTAGTGAG GTTGAGGAAG GAAATTGTGG GGATTTGAAA	1440
TATTCTCTTT ATGTTGTTTC TCTTCTGAGT CATGGTAAAA CAATAAATTA TCATCTCTAG	1500
GTGGCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1540

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Leu	Leu	Leu	Leu	Lys	Pro	Asp	Phe	Phe	Ile	Leu	Leu	Gly	Ser
1					5				10					15	
Glu	Glu	Ser	Arg	Cys	Leu	Val	Asp	Val	Gln	Tyr	Val	Ile	Phe	Phe	Leu
			20					25						30	
Ile	Glu	Cys	Val	His	Leu	Lys	Ser	Ser	Leu	Thr	Phe	Leu	Glu	Arg	Leu
			35				40					45			
Leu	Ser	Ile	Asn	Asn	Gly	Ile	Leu	Glu	Glu	Lys	Trp	Phe	Phe	Lys	Ser
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ANTGACGCCTT TAGCTAGTCC TTCTATCA

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TNCAACAGTAT CAACCAGAAG TGCCAATC

29

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GNAAACAGTAT TAAATTGCAG AGTTCCAG

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CNAATCATCAT CTCGCTTACA CAGTCAGG

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANCGAGACAGA CCAAGGCTCA CAGGTGAA

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GNGGACACACA CTCATAAAAC AGAAAATA

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ANTAACCATAG AGTTTGGCTG GAGACCAC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ANTCTTCCGAT GGCAACACCA GCCTGCTT

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GNTCACCATTT CTGTGTTCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ANATTTAGGCT TATGCTGACC TCGTTGTA

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Gly Asn Ala Ser Tyr Ser Asp Ser Tyr Leu Glu Gly Ile Leu Leu
1 5 10 15
Lys Gly Val Phe Thr Cys Glu Pro Trp Ser Val Ser Val Gly Trp Ser
20 25 30
Thr Ser Val Asp Cys Gly Trp Phe Gln Ser Ala Trp Leu Arg Ser Ser
35 40 45
Thr Glu Gly Ser Thr Gly Ala Ala Leu Trp Gln Arg Leu Arg Arg Glu
50 55 60
Met Asp Gln Pro Thr Pro Gly Thr Trp Leu His Gly Ile Arg Lys Gly
65 70 75 80
Arg Cys Trp Pro Leu Cys Ser Cys Cys Leu Phe Leu Phe Leu Phe Ala
85 90 95
Phe Asp Leu Val Ala Thr Asp Arg Val Ala Arg Asp Leu Val Phe Ser
100 105 110
Ser Arg His Pro Ser Thr Pro Ala Leu Ser Gln Val Ser Cys Cys His
115 120 125
Ala Asn Ala Met Ser Thr Leu Ala Pro Arg Pro Lys Ser Val Gln Arg
130 135 140
Trp Pro Thr Xaa Ser Ser His Tyr Ser Leu Asn Ser Met Tyr His Leu
145 150 155 160
Pro Leu

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Val Gly Gly Pro Phe Leu Pro Pro Thr Ser Val Cys Cys Ser Cys
1 5 10 15
Gln Lys Thr Cys Leu Leu Leu Pro Ala Glu Arg Glu Gln Ser Pro Glu
20 25 30

His His Gln Glu Cys Leu Leu Val Tyr Trp Gln Leu Ala Thr Pro Ser
 35 40 45
 Ser Pro Phe Thr Gln Thr Arg Gly Arg Asp Gly Lys Gly Phe Phe Thr
 50 55 60
 Glu His Ser Gly Thr Pro Tyr Arg Arg Lys Leu Asp Arg Leu Val Asn
 65 70 75 80
 Gly Phe Ser

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTAACCTTCT TCTGCGCGGC TGCAGCTCGG GACTTCGGCC TGACCCAGCC CCCATGGCTT	60
CAGAAGAGCT ACAGAAAGAT CTAGAAGAGG TAAAGGTGTT GCTGGAAAAG GCTACTAGGA	120
AAAGAGTACG TGATGCCCTT ACAGCTGAAA AATCCAAGAT TGAGACAGAA ATCAAGAACA	180
AGATGCAACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG	240
TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT	300
CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA	360
ATGTGCAGGT GCATTTTACA GAGAGGTCAT TTGATCTTTT GGTAAGAAT CTAAATGGGA	420
AGAGTTACTC CATGATTGTG AACAACTCTCT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA	480
AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT	540
GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA	600
CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTTAT GAAGATGGAG	660
ACGATGATAT GAAGCGAACC ATTAATAAAG CCTGGGTGGA ATCAAGAGAG AAGCAAGCCA	720
AAGGAGACAC GGAATTTTGA GACTTTAAAG TCGTTTTGGG AACTGTGATG TGATGTGGAA	780
ATACTGATGT TTCCAGTAAG GGAATATTGG TGAGCTGCAT ATATAAATTT GACAGATAGC	840
TATTTACATA GCCTTCTAAG TAAAGGCAAT GAATTCTCCA TTTCTACTG GAGGATTTAT	900
TTAAATAAAA TATGCTTATT AAACACTCCT GCAAAGATGG TTTTATTAGT ACCCTGGTCA	960

TTTTGTTCAA GGAAGGGTTA TATTGCATTC TCACGTGAAA TATAAAAAGC AAGTCTTGCC 1020
 CAATAAAAAC GCTACATTGT GTGTATTTTT TGTTCAGCTA AGAATTGGAA AAGTATTTGC 1080
 TTGCCTTTTA AGTTACTGAC ATCAGCTTCC ACCAGTGTA AAATTGAGTA AAACCTGAAG 1140
 TTTTGCATAA AATGCAAATC GGTGCCTGTG CTTGAAGGTT GCTGTAGAGC ATCTGACCCC 1200
 TTATTACCAC CTTAAGCAAT GTATATGCCA TGCATTACCA TGCAC TAATT CAATCACAGG 1260
 TGTCTTCTATC TAGATTTAAA TATATTTGTC AATGAATGTG GAATAGAAAA TCTAAACATG 1320
 ACAATAATAG ACATATCTTT GTATGGTACC AGTTAGTTTT GCCGTGGATC AGATGGTTTA 1380
 TAAAAGTAAT AACCATAAAG CAAAAAATAA TTTGAAAGCC CGTCTATTCC TATGCTCAAT 1440
 AAAGTTAAGT TTTTTTTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAAAAA AAAAAAAAAA A 1521

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ala	Ser	Glu	Glu	Leu	Gln	Lys	Asp	Leu	Glu	Glu	Val	Lys	Val	Leu
1				5					10					15	
Leu	Glu	Lys	Ala	Thr	Arg	Lys	Arg	Val	Arg	Asp	Ala	Leu	Thr	Ala	Glu
			20					25					30		
Lys	Ser	Lys	Ile	Glu	Thr	Glu	Ile	Lys	Asn	Lys	Met	Gln	Gln	Lys	Ser
		35					40					45			
Gln	Lys	Lys	Ala	Glu	Leu	Leu	Asp	Asn	Glu	Lys	Pro	Ala	Ala	Val	Val
	50					55					60				
Ala	Pro	Ile	Thr	Thr	Gly	Tyr	Thr	Val	Lys	Ile	Ser	Asn	Tyr	Gly	Trp
65					70					75				80	
Asp	Gln	Ser	Asp	Lys	Phe	Val	Lys	Ile	Tyr	Ile	Thr	Leu	Thr	Gly	Val
			85					90						95	
His	Gln	Val	Pro	Thr	Glu	Asn	Val	Gln	Val	His	Phe	Thr	Glu	Arg	Ser
			100					105					110		

Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Ser Tyr Ser Met Ile
 115 120 125

 Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Gly Ser Ser Lys Lys
 130 135 140

 Val Lys Thr Asp Thr Val Leu Ile Leu Cys Arg Lys Lys Val Glu Asn
 145 150 155 160

 Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu Lys
 165 170 175

 Glu Lys Pro Ser Tyr Asp Thr Glu Thr Asp Pro Ser Glu Gly Leu Met
 180 185 190
 Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys Arg
 195 200 205

 Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Lys Gly
 210 215 220

 Asp Thr Glu Phe
 225

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGCGTCATGC AGTGCGCCGG AGGAACTGTG CTCTTTGAGG CCGACGCTAG GGGCCCGGAA	60
GGGAAACTGC GAGGCGAAGG TGACCGGGGA CCGAGCATTT CAGATCTGCT CGGTAGACCT	120
GGTGCACCAC CACCATGTTG GCTGCAAGGC TGGTGTGTCT CCGGACACTA CCTTCTAGGG	180
TTTTCCACCC AGCTTTCACC AAGGCCTCCC CTGTTGTGAA GAATTCCATC ACGAAGAATC	240
AATGGCTGTT AACACCTAGC AGGGAATATG CCACCAAAC AAGAATTGGG ATCCGGCGTG	300
GGAGAACTGG CCAAGAACTC AAAGAGGCAG CATTGGAACC ATCGATGGAA AAAATATTTA	360
AAATTGATCA GATGGGAAGA TGGTTTGTG CTGGAGGGGC TGCTGTTGGT CTTGGAGCAT	420
TGTGCTACTA TGGCTTGGGA CTGTCTAATG AGATTGGAGC TATTGAAAAG GCTGTAATTT	480
GGCCTCAGTA TGTCAAGGAT AGAATTCATT CCACCTATAT GTACTTAGCA GGGAGTATTG	540
GTTTAACAGC TTTGTCTGCC ATAGCAATCA GCAGAACGCC TGTTCTCATG AACTTCATGA	600

TGAGAGGCTC TTGGGTGACA ATTGGTGTGA CCTTTCAGC CATGGTTGGA GCTGGAATGC	660
TGGTACGATC AATACCATAT GACCAGAGCC CAGGCCCAAA GCATCTTGCT TGGTTGCTAC	720
ATTCTGGTGT GATGGGTGCA GTGGTGGCTC CTCTGACAAT ATTAGGGGGT CCTCTTCTCA	780
TCAGAGCTGC ATGGTACACA GCTGGCATTG TGGGAGGCCT CTCCACTGTG GCCATGTGTG	840
CGCCCAGTGA AAAGTTTCTG AACATGGGTG CACCCCTGGG AGTGGGCCTG GGTCTCGTCT	900
TTGTGTCCTC ATTGGGATCT ATGTTTCTTC CACCTACCAC CGTGGCTGGT GCCACTCTTT	960
ACTCAGTGGC AATGTACGGT GGATTAGTTC TTTTCAGCAT GTTCCTTCTG TATGATACCC	1020
AGAAAGTAAT CAAGCGTGCA GAAGTATCAC CAATGTATGG AGTTCAAAAA TATGATCCCA	1080
TTAACTCGAT GCTGAGTATC TACATGGATA CATTAAATAT ATTTATGCGA GTTGCAACTA	1140
TGCTGGCAAC TGGAGGCAAC AGAAAGAAAT GAAGTGA CTC AGCTTCTGGC TTCTCTGCTA	1200
CATCAAATAT CTTGTTTAAT GGGGCAGATA TGCATTAAAT AGTTTGTACA AGCAGCTTTC	1260
GTTGAAGTTT AGAAGATAAG AAACATGTCA TCATATTTAA ATGTTCCGGT AATGTGATGC	1320
CTCAGGTCTG CCTTTTTTTC TGGAGAATAA ATGCAGTAAT CCTCTCCCAA ATAAGCACAA	1380
AAAAAAAAAA AAAA	1394

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Leu	Ala	Ala	Arg	Leu	Val	Cys	Leu	Arg	Thr	Leu	Pro	Ser	Arg	Val
1				5					10					15	
Phe	His	Pro	Ala	Phe	Thr	Lys	Ala	Ser	Pro	Val	Val	Lys	Asn	Ser	Ile
			20					25					30		
Thr	Lys	Asn	Gln	Trp	Leu	Leu	Thr	Pro	Ser	Arg	Glu	Tyr	Ala	Thr	Lys
		35					40					45			
Thr	Arg	Ile	Gly	Ile	Arg	Arg	Gly	Arg	Thr	Gly	Gln	Glu	Leu	Lys	Glu
	50					55					60				
Ala	Ala	Leu	Glu	Pro	Ser	Met	Glu	Lys	Ile	Phe	Lys	Ile	Asp	Gln	Met

65	70	75	80
Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu	85	90	95
Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys	100	105	110
Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr	115	120	125
Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala	130	135	140
Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp	145	150	155
Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu	165	170	175
Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala	180	185	190
Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr	195	200	205
Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly	210	215	220
Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys	225	230	235
Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe	245	250	255
Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly	260	265	270
Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser	275	280	285
Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val	290	295	300
Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu	305	310	315
Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met	325	330	335
Leu Ala Thr Gly Gly Asn Arg Lys Lys	340	345	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTTTTTTT	TTTTTTTTTG	TTGAGATGGG	GTCTCGCCAT	GTTTCCCACA	CTGATCTTGA	60
ACTCCTGGGC	TCCAGGAATT	CTCCTACTTT	GGCCTCCCAA	AGTGTTGGGA	ATATTGGCAT	120
GAACCACAGC	ACCTGACTTG	CATATTTGTG	AATTCCCCAA	ATTGCTTTTT	TTAAATTGAT	180
TTCTAATTTC	ATTTCATTGT	TATGGGGAAC	ATACTTTGTA	TGGTTTCAAT	GTTTTAAAAAT	240
TAATTGAGAC	TTGTTTTATG	ACTTAGCATA	TGGTCTGTGT	TGAAGAAGGC	TCCATGTACA	300
CTTGAGAATA	ATATGTATAC	TGTGGTTGTT	GGGTGGATTT	TCTATGTATG	TTTARGTGAT	360
ATGGTTTTAT	AGTGTTGTTT	AARTCTTCTA	TTTTCTTCTT	TTTCTGCCCA	GTTTTATTTT	420
TGAAAGCATA	CTGARGTCTC	CAACTCARTG	CCTTAGCCTC	CTGAGCAGTT	GGGACTACAG	480
GCATACGCCA	CTACACCCAG	CAATTTTTTT	GTATTTTTCT	GTAAGACAG	AGTTTCACCA	540
TGTTGCCTAG	GCTGGTCTCA	GATTCCTGGA	CTCAAGTGAT	CTCGATTCCC	GGCCTCTGCC	600
TCCCGGGGTG	CTGGGATTGC	AGGCATGAGC	TACTATGCCT	GGCAAATTTT	ATTTTTTCCTT	660
TTATTTTGTC	ACATAATTAA	AGCTACTCCA	GAATTCCCTT	GATTTCTGCT	TGCCTGGTAT	720
ATCTTTTTTC	CATTTTTTAA	CTGTCAGCCT	TTTTTGTGCC	TGTTAATCTA	AAGTATGTGT	780
TTCGTAGATA	ATATGTAGCT	GGATCATATT	TTAAAAATAT	TTATTCTGCC	AAGCTCTGTC	840
TTTTGATTGG	AGTATTCTTT	CATTTATGTT	TGTAATTACT	GATGAGGGGG	GCACTAATGT	900
CTGCTGTTTT	GCTATTTGTT	TCCCCATGTC	TTATGTCTTC	ATTACTGACT	TTTTTATTAA	960
ACAACTATTT	TCTTGGGTAC	CATTTTAAGT	CCCTCTCCCA	CTCATTTTTT	AATGTTTTTT	1020
TGTGTTTACT	TTGTTTTTTA	TTGTTTGCCC	TGATATTAAA	ATTAACATTT	TACCTTGAAA	1080
TAGTTGGCTT	CAGATTAATA	TCAACTTAGT	TTCAATAGCA	TAGGAAATTT	GCTTCACTAT	1140
ATTTCCATTT	TCTCCCCGTC	CTTTGTGCTA	TTATTACTAT	ACCAATTAGA	TCTCTACACA	1200
ATATAGGCAT	ATCAACACAT	TTTGTAATTA	TTTCCTTATC	CAGTTGTCTT	TTAATATAGA	1260
TCTGTGAAGA	AAAGTATTAC	ACAAATAGAT	CTATTCTGTT	TTTTATAATT	ATTTAATTAC	1320
CTTTGGTGGT	GCTGTTTATT	TTTCATGCAT	TTGAGTTACT	GTCTAGTATT	CATTCATTTT	1380
TCTCTGAATC	ACTCCCTTTA	GTATTGCTTG	TAGGGCAGGT	CTGCTAGCAT	TGAATTCCTT	1440

TAATTTTGT GACTCTGCAA ATGCCATAAT TTCTCTTTTG TTTGTGAAGG ATAGTTTTC	1500
TAGATACAGA ATTTGCAGTT GGCATTCTTT TTAGTTTAGC AGTTTGAAAA TATTTCCTAT	1560
TGTTGGCCGG GCACAGTGGC TCACGCCTGT GGTCTAGCA CTTTGGGAGG CCGAGGCGGG	1620
CGGATCGTCT GGGGTCGGGA GTTCGGGACC GGCCTGGCCA ATATGGTGAG GCCCTGTTTC	1680
TGCTAAAATA TAAAAATTGG CTGGGCATGA TGGCGGGTGC CTCTAGTCCC AGCTGCTCGG	1740
GAGGCTGAGG TGGGGGAGTC GCTTGAGCCC GGGAGATGAT GGCTGTGGTG AGCCGGGATG	1800
GCGCCGCTGC ACTCCGGCCT GGGCGGCTGA GTGAGACTCC ATCCCCGAAA AAAAAAAAAA	1860
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA	1908

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Arg	Gly	Ala	Leu	Met	Ser	Ala	Val	Leu	Leu	Phe	Val	Ser	Pro	Cys
1				5					10					15	
Leu	Met	Ser	Ser	Leu	Leu	Thr	Phe	Leu	Leu	Asn	Asn	Tyr	Phe	Leu	Gly
			20					25					30		
Tyr	His	Phe	Lys	Ser	Leu	Ser	His	Ser	Phe	Phe	Asn	Val	Phe	Leu	Cys
		35					40					45			
Leu	Leu	Leu	Phe	Leu	Leu	Phe	Ala	Leu	Ile	Leu	Lys	Leu	Thr	Phe	Tyr
	50					55					60				
Leu	Glu	Ile	Val	Gly	Phe	Arg	Leu	Ile	Ser	Thr					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTTTTTTTTT	TTTTTCAAT	TTCATTTAGT	TCTGCCCTGA	TCTTG GTTAT	TTCCTTTTTT	60
TCTGCTGGGT	TTGGGTTTGG	TTTGTCTTA	TTTCTCTAGT	TCCTTGAGGT	GTGACCTTAR	120
AATGTCAATT	TGTGCTCTTT	CAATCTTTTT	GATGTAGGCG	TTGAGGGCTG	TGGACTTTTC	180
TCTTG GCACT	CCCTTTGGTG	TATCCCARAG	GTTTTGATAG	GTTGTGTCAT	TATTGCAATT	240
CAGTTTGAAG	AATTTCTTAA	TCTCCACCTT	GATTTTGT TT	TTGACCCAAT	GCTCATTCAG	300
GAGCAGGTTA	TTTACTTTCC	ATGTACTTGC	ATGGCTTTGA	AGCTTCCTTT	TGGAGTTGAT	360
TTCCAGTTTT	ATTCCACTGT	GATTTGAGAG	AGTGCTTTAC	ATAATTTCAA	TTTTCTTAAT	420
TTTATTAAGG	CTCGTTTTAT	GGCCTATAAT	ATGGTCTATC	TTGGAGAAAG	TTCCATGCAC	480
TGTAGAATAG	AATGTGTATT	CTGTGGTTGT	TGGATGAAAT	GTTCTGCATA	TATTCCTAGA	540
TTGCCTCCCC	ACAAAAGGTT	GCATCAATGT	CTGTGTTTCT	CTACACCATC	TCACCCTTGC	600
CAACTTCGGG	TTTCATCAGA	CCTTACTGAT	TGTCAGTATG	ATCTGTGAAA	CAAATCTCTC	660
AGTTTTGATT	TGCATTTTTT	AAATTATGAG	AGCTTGAACA	CCATTTTACA	TGTTTATTGG	720
CTGTTGTTAT	TTCCTTTTTG	AGATCTGTTC	GTTATATGCT	TTGCCCGTTT	TTCTGTTGGG	780
TGGTTATTAT	TTTTCTTATT	GAATGGTATA	AGCTCTTTGT	AAGTTAAGGA	CATTAGCCCT	840
TAGTCAGATA	TTTTGACTTA	GGTTTTAATT	TTTTTCCACA	CAGAAGTTTT	AAGCTCTGTG	900
GCAAATTTAT	CAGTCTTATA	TCACTACAGG	GTTATAAATA	TTAGYTATCA	CTTCGGGTTT	960
GTGTCTTGCT	TAGAAAGCMT	CATTTGAAGA	TTGTAAATGT	TAGTAAGTTT	CCCCATATTT	1020
TCCTCTAGGA	CTTCCATGGT	TTAATTTGTT	TTGTTTAAAY	TAGGAATTGG	CATTCACATC	1080
CTYTTTTGTC	CCAGGTCTCA	GAGGTCCCTT	GTATCTTATA	GAGCAGTATT	GTTTTATGTT	1140
ATTTTCCCAT	GTATAATTTA	AAAACAAAAT	ACGTTGTTCA	AAACAAAATA	CAGTGGCAGC	1200
AGATAATGGC	AGTATCTCTG	TAACTGCTGG	TAAACTGTAT	TTCATAGTGA	AGTGTTTATA	1260
AACTAAAGAG	TCATTGATTT	GGTTTCCTGG	CTAATTAAAA	TCTGAATTCC	ATTTGAAGTT	1320
CCATTGAAAT	CATGGTTTTA	CTCTATAGCA	GTGGATGTTT	TTTCCCAACC	TTTCTGATAT	1380
TTTTTTCCTT	CCTGAGACAG	GGTCTTGCTC	TGTCACCTGG	GATGGAGTGT	AGTTGCACCA	1440
TCAAGGCTTA	CTGCAGTCTC	AACTCTCTGA	GCTCAAGTGA	TCCTGCCACC	TCAGCCTCTT	1500
GAGTAGCAAG	GATTACAGGC	ACCTACCACT	ATGCCTGGCT	AATTTTATA	TTTTTTGTAG	1560
AGATGGATTC	TCACTATGTT	GCCCGGGCTC	ATCTTGA ACT	CGAGCTCAAG	CAATCTGTCC	1620

ATCTTGGCCT	CCCAAAGTGC	TGGGATTATA	GGCGTGAGCC	ACTGCACCTG	GCCCCTTTCT	1680
GATTATTTTA	ATCTATCTTT	AAATGTTCAA	AGTGATTGTC	CTAATTCATT	TAAAGCATAT	1740
TTAGTTTTTT	TTAAATTGAG	TGTATTTTAT	CTAGATATTT	TTAAAAGGCA	GCATCTAACC	1800
TTGGATTTTA	TAAATACATC	TAAATTTGTT	ATTTCCAGAA	TGCTTCAAAA	CAGATCTCTG	1860
TAGCCTCGTG	CTTTGTTATT	GTTAGGTTTT	TTTTTTTTGT	TTTGAGACAG	GGTCTTGCTC	1920
TATCTGGAGT	GCAGTGGCAC	AGTCATAGCT	CACTGTACCC	TCAAACCTCCT	AAACTCAAGT	1980
AATCCTCCCA	TCTCAGCCTC	CTGAGTAGTT	GGGACCACAG	TCATGCACCA	GCATGCCTGG	2040
CTAATTTTTT	AAATTTTGTT	CTTAATAGAG	ACAGAGTCTT	GCTGTGTTGT	TCAGGCTGGT	2100
CTCAAACCTC	TGGGCTCAAG	CGATCCTCCC	ACCTCAGCCT	CCTAAAGTGC	TGAGATTACG	2160
GATGTGAATC	ATTACACCCA	GCCTATTAAT	GGTTTGTAT	AGCAAGTCTT	TTGTGGGTGG	2220
TGGAAAGATG	AAGTGCTGTG	AAATATTGTA	GGAGCAGAAA	CTTGAAATGT	GGCAAAAACC	2280
ACATGGGCAA	AATTTCTGTC	TCTTTTCTTA	TTTTTGCTTT	TTTGTTTAAA	GGTTTTTCTA	2340
TTGGGAAAGC	TACTGATCGG	ATGGATGCTT	TCAGGAAAGC	AAAGAACAGA	GCAGTTCACC	2400
ATTTGCATTA	TATAGAACGA	TATGAAGACC	ATACAATATT	CCATGATATT	TCATTAAGAT	2460
TTAAAAGGAC	GCATATCAAG	ATGAAGAAAC	AACCCAAAGG	TTACGGCCTC	CGCTGCCACA	2520
GGGCCATCAT	CACCATCTGC	CGGCTCATTG	GCATCAAAGA	CATGTATGCC	AAGGTCTCTG	2580
GGTCCATTAA	TATGCTCAGC	CTCACCAGG	GCCTCTTCCG	TGGGCTCTCC	AGACAGGAAA	2640
CCCATCAACA	GCTGGCTGAT	AAGAAGGGCC	TCCATGTTGT	GGAAATCCGG	GAGGAATGTG	2700
GCCCTCTGCC	CATTGTGGTT	GCGTCCCCCC	GGGGGCCCTT	GAGGAAGGAT	CCAGAGCCAG	2760
AAGATGAGGT	TCCAGACGTC	AAACTGGACT	GGGAAGATGT	GAAGACTGCA	CAGGGAATGA	2820
AGCGCTCTGT	GTGGTCTAAT	TTGAAGAGAG	CCGCCACGTA	ACCTCTCTGG	CCTTGTGCAG	2880
CCAGTTCCTG	TGCTGCCCTG	CACCTAGGAG	AGACTCAGCC	CCTCACAGCT	TGGGATGTTA	2940
CCTTGCCTTT	TGTTTGTTTT	GAGGGAAGTT	TAATCTTTAA	ACTCTTTGGA	AATAAATAAT	3000
TATAGCTTTC	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3060
AAAAAAAAAA	AAAAAA					3076

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Gly	Lys	Ile	Ser	Val	Ser	Phe	Leu	Ile	Phe	Ala	Phe	Leu	Phe	Lys
1				5					10					15	
Gly	Phe	Ser	Ile	Gly	Lys	Ala	Thr	Asp	Arg	Met	Asp	Ala	Phe	Arg	Lys
			20					25					30		
Ala	Lys	Asn	Arg	Ala	Val	His	His	Leu	His	Tyr	Ile	Glu	Arg	Tyr	Glu
		35					40					45			
Asp	His	Thr	Ile	Phe	His	Asp	Ile	Ser	Leu	Arg	Phe	Lys	Arg	Thr	His
	50					55					60				
Ile	Lys	Met	Lys	Lys	Gln	Pro	Lys	Gly	Tyr	Gly	Leu	Arg	Cys	His	Arg
65					70					75					80
Ala	Ile	Ile	Thr	Ile	Cys	Arg	Leu	Ile	Gly	Ile	Lys	Asp	Met	Tyr	Ala
				85					90					95	
Lys	Val	Ser	Gly	Ser	Ile	Asn	Met	Leu	Ser	Leu	Thr	Gln	Gly	Leu	Phe
			100					105					110		
Arg	Gly	Leu	Ser	Arg	Gln	Glu	Thr	His	Gln	Gln	Leu	Ala	Asp	Lys	Lys
		115					120					125			
Gly	Leu	His	Val	Val	Glu	Ile	Arg	Glu	Glu	Cys	Gly	Pro	Leu	Pro	Ile
	130					135					140				
Val	Val	Ala	Ser	Pro	Arg	Gly	Pro	Leu	Arg	Lys	Asp	Pro	Glu	Pro	Glu
145					150					155					160
Asp	Glu	Val	Pro	Asp	Val	Lys	Leu	Asp	Trp	Glu	Asp	Val	Lys	Thr	Ala
			165						170				175		
Gln	Gly	Met	Lys	Arg	Ser	Val	Trp	Ser	Asn	Leu	Lys	Arg	Ala	Ala	Thr
		180						185					190		

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGCCAAGTGC GCATGGGGAC GCTATAGCAA TTCGTTTGCT GTCCTTCCTC TCCTTCGAAG 60
ATGACAAGGC CTACCATCGT TTCTTCCTGC CTTTGGGCCG TCAGGCAGTT GGTGTTGGGACC 120
CGCTCCAACC CTCGGTTCTT CCTGCAATAC AGTGGATACA ATTTGTCATG GCTACTCTGA 180
GTGTTATAGG TTCAAGTTCA CTTATTGCCT ATGCTGTATT CCATAATATA CAGAAATCTC 240
CAGAGATAAG ACCACTTTTT TATCTGAGCT TCTGTGACCT GTCCTGGGA CTTTGCTGGC 300
TCACGGAGAC ACTTCTCTAT GGAGCTTCAG TAGCAAATAA GGACATCATC TGCTATAACC 360
TACAAGCAGT TGGACAGATA TTCTACATTT CCTCATTTCT CTACACCGTC AATTACATCT 420
GGTATTTGTA CACAGAGCTG AGGATGAAAC ACACCCAGAG TGGACAGAGC ACATCTCCAC 480
TGGTGATAGA TTATACTTGT CGAGTTGGTC AAATGGCCTT TGTTTTCTCA AGCCTGATAC 540
CTCTGCTATT GATGACACCT GTATTCTGTC TGGGAAATAC TAGTGAATGT TTCCAAAAC 600
TCAGTCAGAG CCACAAGTGT ATCTTGATGC ACTCACCACC ATCAGCCATG GCTGAACTTC 660
CACCTTCTGC CAACACATCT GTC 683

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ala Thr Leu Ser Val Ile Gly Ser Ser Ser Leu Ile Ala Tyr Ala
1 5 10 15
Val Phe His Asn Ile Gln Lys Ser Pro Glu Ile Arg Pro Leu Phe Tyr
20 25 30
Leu Ser Phe Cys Asp Leu Leu Leu Gly Leu Cys Trp Leu Thr Glu Thr
35 40 45
Leu Leu Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn
50 55 60
Leu Gln Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr
65 70 75 80
Val Asn Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr

85

90

95

Gln	Ser	Gly	Gln	Ser	Thr	Ser	Pro	Leu	Val	Ile	Asp	Tyr	Thr	Cys	Arg
			100					105						110	
Val	Gly	Gln	Met	Ala	Phe	Val	Phe	Ser	Ser	Leu	Ile	Pro	Leu	Leu	Leu
		115					120					125			
Met	Thr	Pro	Val	Phe	Cys	Leu	Gly	Asn	Thr	Ser	Glu	Cys	Phe	Gln	Asn
	130					135					140				
Phe	Ser	Gln	Ser	His	Lys	Cys	Ile	Leu	Met	His	Ser	Pro	Pro	Ser	Ala
145					150					155					160
Met	Ala	Glu	Leu	Pro	Pro	Ser	Ala	Asn	Thr	Ser	Val				
			165						170						

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATATGGCTGG	ACGCAGCACA	AATTCCACCA	ACTAAAGCAG	GAGGCTCGGC	GTGATGCAGA	60
TACCCAGACA	CCATTATTAT	GCTCACAGAA	GAGATTCTAT	AGCAGGGGCT	TAAATTCACT	120
GGAATCCACC	CTGACTTTTC	CTGCCAGTAC	TTCTACCATT	TTTGGAACT	ACAATACTGG	180
AACATCCAGG	AAGTGGAGTT	ATTCTACGCT	AATGGATTGG	AAAGAATGTT	GGGAAAGGAC	240
ATCTTAAATC	TTTTCTAACT	ATGCCCTAAA	CTGCAGAACT	CAAAGGAAAT	ATAGTGCCAT	300
TGTTAGTAGT	CATTCTAGAT	GAATTGGGAG	TATCTCTCCA	GTTATTCCCA	GATTCACCTAG	360
TGATCCTTAA	AGTCTCTATT	CAGGGAGAGG	AAGACACTTT	CCATCTCAGA	GATAGACTCG	420
TGTTACCTTG	ATGGATATTG	GATTTGTCTA	AGTCTCTTCT	AGAAAAAATA	AATTCTAGAT	480
TATTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA		524

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCCCGCTACC GGGTTGCGGC CGGAAGCCGG GCGCCGCGGC TCTGCTTCCC TCGGGGATCT	60
GGCGACATGG CCAGAAAGGC TCTCAAGCTT GCTTCGTGGA CCAGCATGGC TCTTGCTGCC	120
TCTGGCATCT ACTTCTACAG TAACAAGTAC TTGGACCCTA ATGACTTTGG CGCTGTCAGG	180
GTGGGCAGAG CAGTTGCTAC GACGGCTGTC ATCAGTTACG ACTACCTCAC TTCCCTGAAG	240
AGTGTCCCTT ATGGCTCAGA GGAGTACTTG CAGCTGAGAT CTAAGGTGCA CCTTCGCTCT	300
GCCAGGCGTC TCTGTGAGCT CTGCTGTGCC AACCGGGGCA CCTTCATCAA GGTGGGCCAG	360
CACCTGGGGG CTCTGGACTA CCTGTTGCCA GAGGAGTACA CCAGCACGCT GAAGGTACTG	420
CACAGCCAGG CTCCACAGAG CAGCATGCAA GAGATCCGCC AGGTCATCCG AGAAGATCTG	480
GGCAAGGAGG TGCTCGTTCT GGCTGTGAAG CAGCTGTTCC CAGAGTTTGA GTTTATGTGG	540
CTTGTGGATG AAGCCAAGAA GAACCTGCCT TTGGAGCTGG ATTCCTCAA TGAAGGGAGG	600
AATGCTGAGA AGGTGTCCCA GATGCTCAGG CATTTTGA CTCTGAAGGT CCCCCGAATC	660
CACTGGGACC TGTCCACGGA GCGGGTCCTC CTGATGGAGT TTGTGGATGG CGGGCAGGTC	720
AATGACAGAG ACTACATGGA GAGGAACAAG ATCGACGTCA ATGAGGTGAG GTCAAGAGCT	780
CAGGGCTGCT GTGCCGGGGA ACGTGGGCTT GGTCAAGGCT GCCCAGGAAG TGCCTGTGTG	840
TCCAGATCTC ACGCCACCTG GGCAAGATGT ATAGTGAGAT GATCTTCGTC AATGGCTTCG	900
TGCACTGCGA TCCCCACCCC GGCAATGTAC TGGTGCGGAA GCACCCCGGC ACGGGAAAGG	960
CGGAGATTGT CCTGTTGGAC CATGGGCTTT ACCAGATGCT CACGGAAGAA TTCCGCTGA	1020
ATTACTGCCA CCTCTGGCAG TCTCTGATCT GGACTGACAG GAAGAGAGTG AAGGAGTACA	1080
GCCAGCGACT GGGAGCCGGG GATCTCTACC CCTTGTTTGC CTGCATGCTG ACGGCGCGAT	1140
CGTGGGACTC GGTCAACAGA GGCATCAGCC AAGCTCCCGT CACTGCCACT GAGGACTTAG	1200
AGATTCGCAA CAACGCGGCC AACTACCTCC CCCAGATCAG CCATCTCCTC AACCACGTGC	1260
CGCGCCAGAT GCTGCTCATC TTGAAGACCA ACGACCTGCT GCGTGGCATT GAGGCCGCCC	1320
TGGGCACCCG CGCCAGCGCC AGCTCCTTTC TCAACATGTC ACGTTGCTGC ATCAGAGCGC	1380
TAGCTGAGCA CAAGAAGAAG AATACCTGTT CATCTTCAG AAGGACCCAG ATCTCTTTCA	1440
GCGAGGCCTT CAACTTATGG CAGATCAACC TCCATGAGCT CATCCTGCGT GTGAAGGGGT	1500
TGAAGCTGGC TGACCGGGTC TTGGCCCTAA TATGCTGGCT GTTCCCTGCT CCACTCTGAG	1560

TGGAATTGCT CTCCCTGCCC CATTCTGGTG TCTTTCCACT CCTCAGCCCC TCATCTTGCC 1620
 TCCACCCAGC TGCTCCATTT TTGCCACATC GTGGCCCGCA GCCCCAGAGT CACTGTCCAT 1680
 GTCACCATCC TCCTCCTCCT TTGGAATCCT CTCCGCACAC TGTGGCCCTT GTCTCAGGGC 1740
 CCACAAGCTG AACTGTGGCA TAGCTCTCTC TTCTTCTCCA AGAAGACTCA GCAGCCTACA 1800
 TTCCCATTC TGGTATGTGC CATTGGGTTG GATGTCCCCA CTACTTCCGT TAACCCTTCC 1860
 CATTGTCAAG ATGTGCCACG GGTGCCACTG GGGGCACACT GAACTTGTAG GGAGTGTGAT 1920
 TTTGTTGGAG GTGCACATGG TCTCTGAATT TGACAGAGAA CACCTTCCCT TTCCTTGCCA 1980
 TGTCACCCTC CAGAGGAAGT CACACCTCAG CGAGGTGGTT TGGCATCTGG GGCCAACTCC 2040
 ATTACAGCTA TGAGCTCACT GCTGTCAGTG ACGTTTGGTG TTTTCTGTAC TGTGTTTCAA 2100
 TAAAAACTCC TTCAAGGTTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2160
 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
 1 5 10 15
 Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
 20 25 30
 Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
 35 40 45
 Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
 50 55 60
 Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
 65 70 75 80
 Arg Leu Cys Glu Leu Cys Cys Ala Asn Arg Gly Thr Phe Ile Lys Val
 85 90 95
 Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr
 100 105 110

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln	
115 120 125	
Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Val Leu Val	
130 135 140	
Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu Val	
145 150 155 160	
Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn Glu	
165 170 175	
Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp Phe	
180 185 190	
Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val Leu	
195 200 205	
Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr Met	
210 215 220	
Glu Arg Asn Lys Ile Asp Val Asn Glu Val Arg Ser Arg Ala Gln Gly	
225 230 235 240	
Cys Cys Ala Gly Glu Arg Gly Leu Gly Gln Gly Cys Pro Gly Ser Ala	
245 250 255	
Cys Val Ser Arg Ser His Ala Thr Trp Ala Arg Cys Ile Val Arg	
260 265 270	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CATGGCGGCT CCCTTGGTCC TGGTGCTGGT GGTGGCTGTG ACAGTGCGGG CGGCCTTGTT	60
CCGCTCCAGT CTGGCCGAGT TCATTTCCGA GCGGGTGGAG GTGGTGTCCC CACTGAGCTC	120
TTGGAAGAGA GTGGTTGAAG GCCTTTCACT GTTGGACTTG GGAGTATCTC CGTATTCTGG	180
AGCAGTATTT CATGAACTC CATTAATAAT ATACCTCTTT CATTTCTTAA TTGACTATGC	240
TGAATTGGTG TTTATGATAA CTGATGCACT CACTGCTATT GCCCTGTATT TTGCAATCCA	300
GGACTTCAAT AAAGTTGTGT TTAAAAAGCA GAAACTCCTC CTAGAACTGG AACAGTATGC	360

CCCAGATGTG	GCCGAACTCA	TCCGGACCCC	TATGGAAATG	CGTTACATCC	CTTTGAAAGT	420
GGCCCTGTTC	TATCTCTTAA	ATCCTTACAC	GATTTTGTCT	TGTGTTGCCA	AGTCTACCTG	480
TGCCATCAAC	AACACCCTCA	TTGCTTTCTT	CATTTTGA	ACTGATAAAG	TTTCATTATC	540
TGTAAAATGG	GGACAGTAAT	TGTACCCACT	TCATGGAATT	ATTGAGAAGA	CTAAATGGCT	600
TAAGGCAGTG	CTTTCCTCAG	TGCTATTTTT	CTTGCCTTAG	CGACATACCA	GTCTCTGAAC	660
CCACTCACCT	TGTTTGTCCC	AGGACTCCTC	TATCTCCTCC	AGCGGCAGTA	CATACCTGTG	720
AAAATGAAGA	GCAAAGCCTT	CTGGATCTTT	TCTTGGGAGT	ATGCCATGAT	GTATGTGGGA	780
AGCCTAGTGG	TAATCATTTG	CCTCTCCTTC	TTCTTCTCA	GCTCTTGGGA	TTTCATCCCC	840
GCAGTCTATG	GCTTTATACT	TTCTGTTCCA	GATCTCACTC	CAAACATTGG	TCTTTTCTGG	900
TACTTCTTGG	CAGAGATGTT	TGAGCACTTC	AGCCTCTTCT	TTGTATGTGT	GTTTCAGATC	960
AACGTCTTCT	TCTACACCAT	CCCCTTAGCC	ATAAAGCTAA	ATCCTGAGAA	ACATCTTTGT	1020
CCTCACCTGC	ATCATCATCG	TCTGTTCCCT	GCTCTTCCCT	GTCCTGTGGC	ACCTCTGGAT	1080
TTATGCAGGA	AGTGCCAACT	CTAATTTCTT	TTATGCCATC	AACTGACCT	TCAACGTGG	1140
GCAGATCCTG	CTCATCTCTG	ATTACTTCTA	TGCCTTCCTG	CGGCGGGAGT	ACTACCTCAC	1200
ACATGGCCTC	TACTTGACCG	CCAAGGATGG	CACAGAGGCC	ATGCTCGTGC	TCAAGTAGGC	1260
CTGGCTGGCA	CAGGGCTGCA	TGGACCTCAG	GGGGCTGTGG	GGCCAGAAGY	TGGGCCAAGC	1320
CCTCCAGCCA	GAGTTGCCAG	CAGGCGAGTG	CTTGGGCAGA	AGAGGTTCGA	GTCCAGGGTC	1380
ACAAGTCTCT	GGTACCAAAA	GGGACCCATG	GCTGACTGAC	AGCAAGGCCT	ATGGGGAAGA	1440
ACTGGGAGYT	CCCCAACTTG	GACCCCCACC	TTGTGGCTCT	GCACACCAAG	GAGCCCCYTC	1500
CCAGACAGGA	AGGAGAAGAG	GCAGGTGAGC	AGGGCTTGTT	AGATTGTGGC	TACTTAATAA	1560
ATGTTTTTTG	TTATGAAGTC	TAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA	1613

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg

1	5	10	15
Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val			
20	25	30	
Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu			
35	40	45	
Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His			
50	55	60	
Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala			
65	70	75	80
Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr			
85	90	95	
Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu			
100	105	110	
Leu Leu Glu Leu Glu Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg			
115	120	125	
Thr Pro Met Glu Met Arg Tyr Ile Pro Leu Lys Val Ala Leu Phe Tyr			
130	135	140	
Leu Leu Asn Pro Tyr Thr Ile Leu Ser Cys Val Ala Lys Ser Thr Cys			
145	150	155	160
Ala Ile Asn Asn Thr Leu Ile Ala Phe Phe Ile Leu Thr Thr Ile Lys			
165	170	175	
Val Ser Leu Ser Val Lys Trp Gly Gln			
180	185		

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACCCTGTC GGTCTTGGAG CGACGACGGC AGAACCAGGG TCCCTGGCGG TGCGGCGGGG	60
CCGGCGGGTG CAGCGGAAGC GGCGGCGGCG GCGGCAGTGA CGTCGCCGGG AACCTAAGG	120
ACTCTGCAAT ATGAATAATT CCCTAGAGAA CACCATCTCC TTTGAAGAGT ACATCCGAGT	180
AAAGGCACGG TCTGTCCCGC AACACAGGAT GAAGGAATTT CTGGACTCAC TGGCCTCTAA	240

GGGGCCAGAA GCCCTTCAGG AGTTCCAGCA GACAGCCACC ACTACCATGG TGTACCAACA	300
GGGTGGGAAC TGCATATACA CAGACAGCAC TGAAGTGGCT GGGTCTTTGC TTGAACTTGC	360
CTGTCCAATC AC	372

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 602 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGAAGCTC GAAATGGAGA AGGTGAACCT TATGACCCAG ATGTGCTCTA CTATATTTTC	60
CTGTGTATTC AAAAGTATCT TTTTGAAAT GGAAGGGTAG ATGACATTTT CTCCGATCTT	120
TATTATGTTC GGTTCACGGA GTGGCTACAT GAAGTTCTGA AGGATGTTCA GCCCCGGGTC	180
ACTCCACTTG GCTATGTCTT GCCCAGCCAC GTGACTGAGG AGATGCTATG GGAGTGCAAG	240
CAGCTTGGGG CTCACTCCCC CTCCACCTTG CTGACCACCC TCATGTTCTT TAATACCAAG	300
TAAGTGTTC AGAGGCTCCA CTGCTGGCAT CTGTCCAGTG AAGAGTGTGG AAACCTATCCA	360
AGAGGCCCTTC TGAATTCCTC TGACATATAT TTGAGAACT GGGCTACTGA AAGCCCTAAC	420
CCCACTTGGC TGCATTTTAT TTGGTAACCA GTGAGGCAAA CACCCTTGCC AGACCCCTAC	480
CATCCATCTT GATGTGGTTC CTGCACTGGA CACTGCTTGG GTACGGGCCT GCCCAGATCT	540
TGGGAATGTG GGCAGTGGCT CCTCTGAAGC ACCAGTGGGC AGAGGATGAG TCATGGTATC	600
CT	602

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Trp Phe Leu His Trp Thr Leu Leu Gly Tyr Gly Pro Ala Gln Ile
 1 5 10 15
 Leu Gly Met Trp Ala Val Ala Pro Leu Lys His Gln Trp Ala Glu Asp
 20 25 30
 Glu Ser Trp Tyr Pro
 35

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGAAAGGG CTTGGACTGT GAAAAGAAAT GTGGCCCCTT TCCATCTTCA AGAGAGATGG	60
AATTAATGAT GGATGGACCC TGGAGGGAAT CTCCCCAGCC GACTTCCACT GGGCTGACAG	120
ACTTIGCTGA CCACAGGGGA ACGATGTTCT TTTCTTTCTT CATGATCAGA CATAAACTTA	180
GCATTTTAAT GGAAGAAAAA TGAGGGGAAC TTCAATTATG ATTTATTAAA GACAATTTCT	240
ATTACACCTT CCTTTATGAC AAGTGACATT TTAGATGTAA AAGTAAAAAC TTTACCATGC	300
CTTTTTTTTT TTTGTTGGCC TAACATTGAG GCCTTAAAAC CTGAGGCTCC TGTGCCTGAT	360
GGAATTCTTG TAACATACAC TTGTGTATCA TATAAGATA CCACTCTGTT TCTCTTATGT	420
ATTCTTACTC TAGTTGTTTA TTAAGAATGA CAAGCACGTC TTTTCAACAA AAAAAAAAAA	480
AAA	483

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGATTTCGCT GCTGGAGTGC TGGATGGAGC CTTTCTCTGC CCTCTGTGAC ATTTCCAATT	60
TTAGATAATG CCTCACATCT CTGTCCCCC GGGACCCCT GGAGCCCCCA TGATCCCTAA	120
GAAGACAGCT TGAACCTAGA TCTACCCCC AGGATGTTGC GGAGGCTGCT GGAGCGGCCT	180
TGCACGCTGG CCCTGCTTGT GGGCTCCCAG CTGGCTGTCA TGATGTACCT GTCACTGGGG	240
GGCTTCCGAA GTCTCAGTGC CCTATTTGGC CGAGATCAGG GACCGACATT TGACTATTCT	300
CACCCTCGTG ATGTCTACAG TAACCTCAGT CACCTGCCTG GGGCCCCAGG GGGTCCTCCA	360
GCTCCTCAAG GTCTGCCCTA CTGTCCAGAA CGATCTCCTC TCTTAGTGGG TCCTGTGTCG	420
GTGTCCTTTA GCCCAGTGCC ATCACTGGCA GAGATTGTGG AGCGGAATCC CCGGGTAGAA	480
CCAGGGGGCC GGTACCGCCC TGCAGGTTGT GAGCCCCGCT CCCGAACAGC CATCATTGTG	540
CCTCATCGTG CCCGGGAGCA CCACCTGCGC CTGCTGCTCT ACCACCTGCA CCCCTTCTTG	600
CAGCGCCAGC AGCTTGCTTA TGGCATCTAT GTCATCCACC AGGCTGGAAA TGGAACATTT	660
AACAGGGCAA AACTGTTGAA CGTTGGGGTG CGAGAGGCC TCGTGATGA AGAGTGGGAC	720
TGCCTGTTCT TGCACGATGT GGACCTCTTG CCAGAAAATG ACCACAATCT GTATGTGTGT	780
GACCCCCGGG GACCCCGCCA TGTTGCCGTT GCTATGAACA AGTTTGGATA CAGCCTCCCCG	840
TACCCCCAGT ACTTCGGAAG AGTCTCAGCA CTTACTCCTG ACCAGTACCT GAAGATGAAT	900
GGCTTCCCCA ATGAATACTG GGGCTGGGGT GGTGAGGATG ACGACTTGCT ACCAGGGTGC	960
GCCTGGCTGG GATGAAGATC TCTCGGCCCC CCACATCTGT AGGACACTAT AAGATGGTGA	1020
AGCACCGAGG AGATAAGGGC AATGAGGAAA ATCCCCACAG ATTTGACCTC CTGGTCCGTA	1080
CCCAGAATTC CTGGACGCAA GATGGGATGA ACTCACTGAC ATACCAGTTG CTGGCTCGAG	1140
AGCTGGGGCC TCTTTATACC AACATCACAG CAGACATTGG GACTGACCCT CGGGGTCCTC	1200
GGGCTCCTTC TGGGCCACGT TACCCACCTG GTTCCTCCCA AGCCTTCCGT CAAGAGATGC	1260
TGCAACGCCG GCCCCAGCC AGGCCTGGGC CTCTATCTAC TGCCAACCAC ACAGCCCTCC	1320
GAGGTTCACT CTGACTCCTC CTTCTGTCT ACCTTAATCA TGAAACCGAA TTCATGGGGT	1380
TGTATTCTCC CCACCCTCAG CTCCTCACTG TTCTCAGAAG GATGTGAGGG AACTGAACTC	1440
TGGTGCCGTG CTAGGGGGTA GGGGCCTCTC CCTCACTGCT GGACTGGAGC TGGGCTCCTG	1500
TAGACCTGAG GGTCNTCTY TCTAGGTCTC CTGTAGGGCT TAKGACTGTG AATCCTTGAT	1560
GTCATGATTT TATGTGACGA TTCCTAGGAG TCCCTGCCCC TAGAGTAGGA GCAGGGYTGG	1620
ACCCAAGCC CNTCCYTYTT CCATGGAGAG AAGAGTGATC TGGYTTCTCC TCGGACCTCT	1680
GTGAATATTT ATTCTATTTA TGGTTCCCGG GAAGTTGTTT GGTGAAGGAA GCCCCCCCC	1740

TGGGCATTTT CTGCCTATGC TGAATAGCT CCCTCTTCTG GTCCTGGCTC AGGGGGCTGG 1800
 GATTTTGATA TATTTTCTAA TAAAGGACTT TGTCTCGCAA AAAAAAAAAA AAA 1853

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Leu	Arg	Arg	Leu	Leu	Glu	Arg	Pro	Cys	Thr	Leu	Ala	Leu	Leu	Val	1	5	10	15
Gly	Ser	Gln	Leu	Ala	Val	Met	Met	Tyr	Leu	Ser	Leu	Gly	Gly	Phe	Arg	20	25	30	
Ser	Leu	Ser	Ala	Leu	Phe	Gly	Arg	Asp	Gln	Gly	Pro	Thr	Phe	Asp	Tyr	35	40	45	
Ser	His	Pro	Arg	Asp	Val	Tyr	Ser	Asn	Leu	Ser	His	Leu	Pro	Gly	Ala	50	55	60	
Pro	Gly	Gly	Pro	Pro	Ala	Pro	Gln	Gly	Leu	Pro	Tyr	Cys	Pro	Glu	Arg	65	70	75	80
Ser	Pro	Leu	Leu	Val	Gly	Pro	Val	Ser	Val	Ser	Phe	Ser	Pro	Val	Pro	85	90	95	
Ser	Leu	Ala	Glu	Ile	Val	Glu	Arg	Asn	Pro	Arg	Val	Glu	Pro	Gly	Gly	100	105	110	
Arg	Tyr	Arg	Pro	Ala	Gly	Cys	Glu	Pro	Arg	Ser	Arg	Thr	Ala	Ile	Ile	115	120	125	
Val	Pro	His	Arg	Ala	Arg	Glu	His	His	Leu	Arg	Leu	Leu	Leu	Tyr	His	130	135	140	
Leu	His	Pro	Phe	Leu	Gln	Arg	Gln	Gln	Leu	Ala	Tyr	Gly	Ile	Tyr	Val	145	150	155	160
Ile	His	Gln	Ala	Gly	Asn	Gly	Thr	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	165	170	175	
Val	Gly	Val	Arg	Glu	Ala	Leu	Arg	Asp	Glu	Glu	Trp	Asp	Cys	Leu	Phe	180	185	190	
Leu	His	Asp	Val	Asp	Leu	Leu	Pro	Glu	Asn	Asp	His	Asn	Leu	Tyr	Val	195	200	205	

Cys Asp Pro Arg Gly Pro Arg His Val Ala Val Ala Met Asn Lys Phe
 210 215 220
 Gly Tyr Ser Leu Pro Tyr Pro Gln Tyr Phe Gly Arg Val Ser Ala Leu
 225 230 235 240
 Thr Pro Asp Gln Tyr Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp
 245 250 255
 Gly Trp Gly Gly Glu Asp Asp Asp Leu Leu Pro Gly Cys Ala Trp Leu
 260 265 270
 Gly

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGATAAAGTA AGTGCTGTTT GGGCTAACAG GATCTCCTCT TGCACTCTGC AGCCCAGGAC	60
GCTGATTCCA GCAGCGCCTT ACCGCGCAGC CCGAAGATTC ACTATGGTGA AAATCGCCTT	120
CAATACCCCT ACCGCCGTGC AAAAGGAGGA GCGCGGGCAA GACGTGGAGG CCCTCCTGAG	180
CCGCACGGTC AGAACTCAGA TACTGACCGG CAAGGAGCTC CGAGTTGCCA CCCAGGAAAA	240
AGAGGGCTCC TCTGGGAGAT GTATGCTTAC TCTCTTAGGC CTTTCATTCA TCTTGGCAGG	300
ACTTATTGTT GGTGGAGCCT GCATTTACAA GTACTTCATG CCCAAGAGCA CCATTTACCG	360
TGGAGAGATG TKCTTTTTTTG ATTCTGAGGA TCCTGCAAAT TCCCTTCGTG GAGGAGAGCC	420
TAACTTCCTG CCTGTGACTG AGGAGGCTGA CATTCGTGAG GATGACAACA TTGCAATCAT	480
TGATGTGCCT GTCCCCAGTT TCTCTGATAG TGACCCCTGCA GCAATTATTC ATGACTTTGA	540
AAAGGGAATG ACTGCTTACC TGGACTTGTT GCTGGGGAAC TGCTATCTGA TGCCCCTCAA	600
TACTTCTATT GTTATGCCTC CAAAAATCT GGTAGAGYTC TTTGGCAAAC TGGCGAGTGG	660
CAGATATCTG CYTCAAACCT ATGTGGTTTCG AGAAGACCTA GTTGCTGTGG AGGAAATTCG	720
TGATGTTAGT AACCTTGGCA TCTTTATTTA CCAACTTTGC AATAACAGAA AGTCCTTCCG	780
CCTTCGTGCGC AGAGACCTCT TGCTGGGTTT CAACAAACGT GCCATTGATA AATGCTGGAA	840

Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr	Lys	Tyr	Phe	Met	Pro	65	70	75	80
Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Xaa	Phe	Phe	Asp	Ser	Glu	Asp	85	90	95	
Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Asn	Phe	Leu	Pro	Val	Thr	100	105	110	
Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp	Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	115	120	125	
Pro	Val	Pro	Ser	Phe	Ser	Asp	Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	130	135	140	
Phe	Glu	Lys	Gly	Met	Thr	Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	145	150	155	160
Tyr	Leu	Met	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	165	170	175	
Val	Glu	Xaa	Phe	Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Xaa	Gln	Thr	180	185	190	
Tyr	Val	Val	Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	195	200	205	
Ser	Asn	Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	210	215	220	
Phe	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala	225	230	235	240
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile	Val	245	250	255	
Glu	Thr	Lys	Ile	Cys	Gln	Glu										260			

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TNCACATTCTC AGTGGGAACT TGATGAAC

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ANATATAGGTG GAATGAATTC TATCCTTG

29

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GNTATAGTAAT AATAGCACAA AGGACGGG

29

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TNGCCAGGAAA CCAAATCAAT GACTCTTT

29

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNTAATTGACG GTGTAGAGAA ATGAGGAA

29

- (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANAAATGGAGC AGCTGGGTGG AGGCAAGA

29

- (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TNCGGAGATAC TCCCAAGTCC AACAGTGA

29

- (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GNTTAGGGCTT TCAGTAGCCC AGTTTCTC

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ANTGACAGGTA CATCATGACA GCCAGCTG

29

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CNGGATGTTAG GTGATATATT CATGCTGC

29

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly Glu Val Lys Ser Ser Gly Leu Leu Cys Arg Gly Thr Trp Ala Trp
1 5 10 15

Ser Arg Leu Pro Arg Lys Cys Leu Cys Val Gln Ile Ser Arg His Leu
20 25 30

Gly Lys Met Tyr Ser Glu Met Ile Phe Val Asn Gly Phe Val His Cys
35 40 45

Asp Pro His Pro Gly Asn Val Leu Val Arg Lys His Pro Gly Thr Gly
50 55 60

Lys Ala Glu Ile Val Leu Leu Asp His Gly Leu Tyr Gln Met Leu Thr
65 70 75 80

Glu Glu Phe Arg Leu Asn Tyr Cys His Leu Trp Gln Ser Leu Ile Trp
85 90 95

Thr Asp Arg Lys Arg Val Lys Glu Tyr Ser Gln Arg Leu Gly Ala Gly
100 105 110

Asp Leu Tyr Pro Leu Phe Ala Cys Met Leu Thr Ala Arg Ser Trp Asp
115 120 125

Ser Val Asn Arg Gly Ile Ser Gln Ala Pro Val Thr Ala Thr Glu Asp
130 135 140

Leu Glu Ile Arg Asn Asn Ala Ala Asn Tyr Leu Pro Gln Ile Ser His
145 150 155 160

Leu Leu Asn His Val Pro Arg Gln Met Leu Leu Ile Leu Lys Thr Asn
165 170 175

Asp Leu Leu Arg Gly Ile Glu Ala Ala Leu Gly Thr Arg Ala Ser Ala
180 185 190

Ser Ser Phe Leu Asn Met Ser Arg Cys Cys Ile Arg Ala Leu Ala Glu
195 200 205

His Lys Lys Lys Asn Thr Cys Ser Phe Phe Arg Arg Thr Gln Ile Ser
210 215 220

Phe Ser Glu Ala Phe Asn Leu Trp Gln Ile Asn Leu His Glu Leu Ile
225 230 235 240

Leu Arg Val Lys Gly Leu Lys Leu Ala Asp Arg Val Leu Ala Leu Ile
245 250 255

Cys Trp Leu Phe Pro Ala Pro Leu
260

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2355 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCTTTTTTT TTTTTTTTTT TTCAGAAGGA GGAAGCTCAT TATGTTTGGA TCACCCACAG 60
CTATAGATTC TAAAAATATT TTGGCTTTTT TTGAGGTGCT TTAGTAAAAT ATAACCCCAA 120
ATGATTCACT TGGACAAGTG GTCTTAACAG CAAGGAAAAC AAACACTTTA TGAAAACAGC 180
TATAAGCCTT CTGTCTTTTA TCTTTACTAT TTTCTCCGAG TCTGGCATGA AACAGATACA 240
CAGCAGCCTC CACAGGGGGT TAAGTARAGA ACCATCCAAG CATCACAGAG TGTCATCCAG 300
AATTCTGATG ACTTCCATTC GTTGACTCTG ATGCACAATA TGCCTGGCTT GGGATGCAGC 360
GACCATGATG CCCCTCCCAG AACAGACACT TGCAGAGTGT TCCAGGAACA GCAGCTCCCT 420
CCAGCCCCCA GCACAAGATG CACACATCTC AGAACAAGCC TCCATCCTTT TCCTAGAGAA 480
CTGAGCATAA ATAAC TTGTT CTATATCTGG CTCCAAGTCC ATTTCTGTTC TGTCTTGAG 540
TAGAGTCTTA GCTCCCAAGT TGTTTTAGGT CAACTTTCAG CACCTACTTC AGCTCACTTG 600
TTTGATTTAC TAAGCTCTTG CTTCTGTATA TTATCAAATG TAGGGATGTA GGGAGAATAA 660
AAGGATCTAG ATACTTGCTT TTAGGAGAGA TTAGAACAAA GCTGAAGGTG GAGGCATTAG 720
TTCCTAGGTC TTCAGATCTC AGAGCAAAGG ACCCACTCTG GAGCCTAAAT TCTATGAGAG 780
ACCACAGAGC AGCCTGAAAT CCAAAGGAGT TTTACACAGG AAAAAAAAAA TACTGTGAGG 840
ACTTACACTA AATAATAATG TTGTTTTGAA TGGGGTTGTG GGTAATTCCT ATATTCTTCT 900
TTATAACTTT TGTACTTTTC AAATTCCCTA ATGTGAACTC ACTACTTAGT AGGTCTGTAA 960
GCTTAAACAT TACTATGGCT TGGAATCTCA TTTCAAAAAA TCTTTAAAAT GGGGACAAGA 1020
GTAAAAATTT CTTAGCTTCT ATGGAAGAAT AAAATGAAAT TATAATGATA CAGTGCCTGG 1080
CATGTTGTGG TCGCTCAATA AACACTGCTT TCCTCCCCAT TGTCTCCTC TTTATTCTGT 1140
TTCATTACAA GGTCAGCAGA TTGAATCAGG ACCAGCTGGG AGGGCTACTT CTATGAGAGA 1200
AGATCTGTCC ACAGTCATGG TTTTCAATGT TTAGTGCACC AGAATCACCT TGAGGGTTTG 1260
TTAAACAGA CTGCTGAACA TAACACATCT ATGAGAATGG CAAAATCCA GAACACCAAA 1320
TGCTGGTGAG GATGTGGAGC AATAAAAACT CTCATTTATT GCTGATGGCA ATGCAAAATG 1380

GTACAGCCAC TTTGGAAGAC AATTTGCCAA ATTTTACAA AACTAAGTGT ACTCTTACCA	1440
TACAATCTAG CAATCATGCT CCCTGGTATT TACCTAAAGG AGTTAAAAAC TTATGTCTAG	1500
ACAGAAACCT GCATATGAAT GTTTATAGCA GTTTTTTTCA TAATTGCTAA ACTTTGGAAG	1560
TAACCAAGAT GCCCTTCAGC AGGTGAATGG ACAAATAAAC TGCAGTAGAT GCAGACAGTG	1620
GAATATCATT CTAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAATT AAAGAAAGTC	1680
AGGATAAAAA TTTTAAAAAG CAGGCCACTG TCAGCAAAGC CTGGAGAAGT GGGGCCGGAG	1740
GYTCCGCCCC CATCATGTGC CTGCCACCCC TTCCCAGTCA TCCCTTTAYT CTTACAGTAG	1800
CAAATAAGAC CCCTGTCTAA TGGGGGGAGA CAAATGTGTA GACCCTTAGC CACCTTGGCC	1860
AGGGCTGACT CCTTAAATTT CTGGATGATG ATGATTGTTA TTTAATAGCC AGAGGCTCAT	1920
ATAATTGGCC TCTTTGGAAG AGGCCTCATG GCCTCCTTAC TCTCACCAA GCAATTTTTC	1980
CCTCAGGGGG GCTCCCATCT TCTTACACAG AGAGGCAGCT GAGGCAGGAC AGTGGGGCTA	2040
ACTGTAGACC AGGCGAGGGC ACGGGCTGCT GGGGTGGCCC TGCTTCCCCA GTGTACATAT	2100
TGTATCTGTG TAACATTTTG TATATTCCAG GGGTAGGGCC GCCCCCTGTA TCATACCTAG	2160
CAGAGGTTGG AGCTGGCACA TGGGGAGGAG GTTCTAATAA TTATTGGGG CTGGGAAACT	2220
TATTTATTGA TAGCATAGGA CAGAGGAAGG AGGCGGGGAT GGGGTCGTGG CGCCCTGGTG	2280
ATGCGACTCC TGTTTATTTT GCTTTTATT TCGGAATAAA TGGATTTAGC CATAAAAAAA	2340
AAAAAAAAAA AAAAA	2355

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Thr	Ala	Ile	Ser	Leu	Leu	Ser	Phe	Ile	Phe	Thr	Ile	Phe	Ser
1				5					10					15	
Glu	Ser	Gly	Met	Lys	Gln	Ile	His	Ser	Ser	Leu	His	Arg	Gly	Leu	Ser
			20					25					30		
Xaa	Glu	Pro	Ser	Lys	His	His	Arg	Val	Ser	Ser	Arg	Ile	Leu	Met	Thr
			35				40					45			

Ser Ile Arg
50

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCGCCCTTTC GGTCAACATC GTAGTCCACC CCCTCCCCAT CCCCAGCCCC CGGGGATTCA 60
GGCTCGCCAG CGCCCAGCCA GGGAGCCGGC CGGGAAGCGC GATGGGGGCC CCAGCCGCCT 120
CGCTCCTGCT CCTGCTCCTG CTGTTCGCCT GCTGCTGGGC GCCCGGCGGG GCCAACCTCT 180
CCCAGGACGA CAGCCAGCCC TGGACATCTG ATGAAACAGT GGTGGCTGGT GGCACCGTGG 240
TGCTCAAGTG CCAAGTGAAA GATCACGAGG ACTCATCCCT GCAATGGTCT AACCCCTGCTC 300
AGCAGACTCT CTACTTTGGG GAGAAGAGAG CCCTTCGAGA TAATCGAATT CAGCTGGTTA 360
CCTCTACGCC CCACGAGCTC AGCATCAGCA TCAGCAATGT GGCCCTGGCA GACGAGGGCG 420
AGTACACCTG CTCAATCTTC ACTATGCCTG TGCGAACTGC CAAGTCCCTC GTCACTGTGC 480
TAGGAATTCC ACAGAAGCCC ATCATCACTG GTTATAAATC TTCATTACGG GAAAAAGACA 540
CAGCCACCTT AAAGTGTCAG TCTTCTGGGA GCAAGCCTGC AGCCCGGCTC ACCTGGAGAA 600
AGGGTGACCA AGAACTCCAC GGAGAACCAA CCCGCATACA GGAAGATCCC AATGGTAAAA 660
CCTTCACTGT CAGCAGCTCG GTGACATTCC AGGTTACCCG GGAGGATGAT GGGGCGAGCA 720
TCGTGTGCTC TGTGAACCAT GAATCTCTAA AGGGAGCTGA CAGATCCACC TCTCAACGCA 780
TTGAAGTTTT ATACACACCA ACTGCGATGA TTAGGCCAGA CCCTCCCCAT CCTCGTGAGG 840
GCCAGAAGCT GTTGCTACAC TGTGAGGGTC GCGGCAATCC AGTCCCCCAG CAGTACCTAT 900
GGGAGAAGGA GGGCAGTGTG CCACCCCTGA AGATGACCCA GGAGAGTGCC CTGATCTTCC 960
CTTTCCTCAA CAAGAGTGAC AGTGGCACCT ACGGCTGCAC AGCCACCAGC AACATGGGCA 1020
GCTACAAGGC CTACTACACC CTCAATGTTA ATGACCCCAG TCCGGTGCCC TCCTCCTCCA 1080
GCACCTACCA CGCCATCATC GGTGGGATCG TGGCTTTCAT TGTCTTCCTG CTGCTCATCA 1140
TGCTCATCTT CCTCGGCCAC TACTTGATCC GGCACAAAGG AACCTACCTG ACACATGAGG 1200
CAAAAGGCTC CGACGATGCT CCAGACGCGG ACACGGCCAT CATCAATGCA GAAGGCGGGC 1260

AGTCAGGAGG GGACGACAAG AAGGAATATT TCATCTAGAG GCGCCTGCCC ACTTCCTGCG	1320
CCCCCAGGG GCCCTGTGGG GACTGCTGGG GCCGTCACCA ACCCGGACTT GTACAGAGCA	1380
ACCGCAGGGC CGCCCCTCCC GCTTGCTCCC CAGCCCACCC ACCCCCCTGT ACAGAATGTC	1440
TGCTTTGGGT GCGGTTTTGT ACTCGGTTTG GAATGGGGAG GGAGGAGGGC GGGGGGAGGG	1500
GAGGGTTGCC CTCAGCCCTT TCCGTGGCTT CTCTGCATTT GGGTTATTAT TATTTTTGTA	1560
ACAATCCCAA ATCAAATCTG TCTCCAGGCT GGAGAGGCAG GAGCCCTGGG GTGAGAAAAG	1620
CAAAAAACAA ACAAAAAACA AAACCCTGGA GTGTTAGGAG GAGAGTGAAG GTAGAGGGGT	1680
GAGGAAGGGT AAGGGGCAGG GCTGGTTTCA GCTGGGGGCT CTCACCAGCC CTCCTTTCAG	1740
CCTCTACAAC AGAGCAGCTT CCCAGACTTC TCCAGGAACC CAGAAACGGG ATGGTTGTCTG	1800
GCAAAGGTTG GGAGTGGCTT TTCCTCTGGT AGCCACACAC CTGAGCACTA CGGACAGGGA	1860
GGCAGGTGCC ACCTTGACAC CTCTCTTCCA TAGCAATGGG AAAGTGATGA GTGCGGGAGT	1920
CCTGAGGAGA TGTGGCCTGC AGACAACATG CAGCCATGCA GGGACCCAGG ACTGTAACTT	1980
GGGGAGGACG CGGGTCCCTG CAAGGAAGAG TAGATTTGGA GAGGAAGGAT GGAGGTGGAC	2040
TCTCACCCCA TTCCCCCGG AAATGAACAA AGCCGGGCCC TTTCCATAGG AACTGCCCTT	2100
GGAGATAGCA GAGTGTGGCT GCCCCTCCTT GCTCCAGCAG CAGTGGGAGA GGCAGTCTC	2160
TGGGGCCTGA ACTGCCTCTG CTTCCCCCCC TGAGGGGCCC CTCACTCTTA CCAAGACTC	2220
TGGATTGTTG CACGGCAACC ACTCCTCCCA TGGCATTGCT CAGCAACTAC TTCTCCCTTC	2280
CCGGCCACCC TGTGCCCCCT TCCTGGTCCC AACGCCAGCC CTTCATCCTT CCTCCCTCAG	2340
CAGCCAGGCA GACATAACAA CAAACTACT AAAAGGAGCT TCAAAAAAAAA AAAAAAAAAA	2400
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2460
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA	2496

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala

305		310		315		320
Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile						
		325		330		335
Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly						
		340		345		350
His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys						
		355		360		365
Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu						
		370		375		380
Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile						
		385		390		395

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGCCAAAGA GGCCTACCAG CTGCTGTTGA CCGCTGGACT CACAAACCTT TCTTTCTACT	60
CTTGTTTTTC ATTCACTTTG GGTCATTTTT CAGTGTGAT GGGGACGTAA TAAAGCACGG	120
TAAGAAAATC CGTGAATTCC GTCAGAGCAG TCGTCCAGAG GGAAGGCGCG CCCGGCGTAG	180
GGAGGTCAGA GCTCATGTTA GCTATGAACA CAGGTCACAG GGGCGTACGG CGATGGGAAA	240
CACTGAGATG CTCAATATAT TGATTATTTA ATAGTGTTTA GCAAATGGT CTTTTTTTAT	300
TCCTTAAATC AACTGAAACT CACTTCACGT CTCTTCCTT GTAGAGCATC ATGCTTATTT	360
CTGGCTCACT CACATCTTTG TCTCGGGAGT TCTCTGCCGA GCCATTGCCC CCTACAGCAG	420
AGAGCACAGC TGGCTGCACT AGTGCTGAAG GAGCCAGCCC CAGAGCAGGG CATTTCAGG	480
GGCTCTTGTC CCAGAGCGGC AGGCGTTGTG TGCAGAGAAC GCCCCTCCCA CGCAGCACAG	540
AGAACGCGGG GTGGGTGTGT GGCTCCGGGC CTGTGGGGCT TAGGCTGCCT GAACCACCGC	600
CGACTGGCAC CATGACTCGG CATTCTGGA AGTGCCTTAC CAAGTTGTTG TTGTTGTTTT	660
GTTGTTTTTTT AAGAGACGGG CTTGCTCTAT CATCCAGGCT CGAGTGCAAT GGCACAGTCA	720
CAGCTCACTG CAGCCTTGAA CTCGTGGGCT CAAGCCATCC TCCTGTGTCA GCCTCCCCAG	780

TACCTGGGAC	TGTGGGCATG	AGCACTGCGC	CTGGCAGCTG	TATCAGTGTT	GACTCCACAT	840
TTTAATAGTT	GCTTCTTGAA	ATTAAAATGC	TTTGATTGAG	CCTTCAAGCC	ATCAGGAAAG	900
TTTGCCCCCTC	TGAGTCACAC	CTGGTGGTCT	CCAGGGTTCC	TGCCCCCTCCC	TCCTGAGCCA	960
GCTCCTCAGA	GCGGATAGAG	GCAGGACCCC	CACCCAGGTC	TTGAGACCCC	CCTGCCCCGC	1020
ACTCCCCCGG	AGACGGGCTA	CCCCTGCAGA	TGCAGATAGT	CAAAGCTCAG	GTTTCTTCCA	1080
AAGCTTTTAA	AAAGATATTG	TACCTTGAGC	ACTTTAAAAA	TGTCTTAAAA	TTGCCATACA	1140
GGCTCTTAAA	AGCTTATACG	TTTAAACTGT	TGATAGATGG	GCCTTTACTA	AAATGCATTC	1200
ATTTATTTTC	CTAATCCCTT	GGTTGTAAAA	TAATTCTGGG	GAAGGGCCCC	GAGCACGACA	1260
GCCGCAGTCT	CCACCCAGAA	CCAGAGAGTC	CCCCCAACC	CGGGATGTAC	CCTCTGGCCA	1320
CACCAGGGAC	CCTGCCAGAG	GCCGCAGACT	GGCAGCAGCA	GCCTCCCCAC	ACAGTGGGGG	1380
AAGGTCAGTG	TGATGCCTTC	AGGCCCCGTC	TCCTGCCAGG	GCTCTCCCTC	CAGCCTACAT	1440
AGGGCCTCAG	AGAAATGCAT	TTTTAGTTCT	GGCTTTGGCC	CAGCCCAGGG	CAAGGCAGGA	1500
AACTCTCCAG	CGTGAGTCCG	TGAGGGCCAA	GAAGTCCCGC	CCTGTTCTGG	GGGAGGACCT	1560
GGCTTTTCTG	GTGTCTCTGG	TGCCCCGAGAG	CCCGGTGCTG	CCATCTTTAG	TGAAAGAGTA	1620
AATGGTGGCC	GAGGGCTCCT	TTTGTGAGGG	ATGTGCCTTG	GTGAAGAAGG	CATGTTCCCT	1680
GCCGTGAAGA	TACTTGGAAG	CTCTGGGTGG	AGAGGGAAAA	GGGATACCCC	TGGTGCTCCC	1740
TGGGCCTGGC	GGAAGGCTAG	GAGGAAGGAC	AGCTGAGGTG	AGGACTGAGT	GGGGCAGGTA	1800
TCACCCTGAC	AAACAGTTTG	GGAAGATCAG	GAAAGGCAGG	TGAGACCTGG	TGCAGAATCC	1860
AGGTTGGGTA	ATAGATACAT	CGTCGAAGAT	GTAGCAAGCA	AAGTAATATA	CTCAACTCTG	1920
GAACATTGCA	CAGAAGCTTT	TAAAGCACTC	TGTGACACTT	TTTGTAATGA	GGGATCTGAA	1980
GGAAACGGCC	CCAGAGTCAC	CCATCCCCAC	GGGTCTGGTT	GGCGGGGCTG	GTGCCTTTCT	2040
TCTGCACTCA	GTCACCATGG	CTCCGTCTGT	CAAACCTAAC	TCTTTTTTTT	TTTTTTTTTTC	2100
TTCTCTTGGT	GTGGTAATTT	GTTTGAAGAG	CCACTCCATC	CCCAAATTCA	AGATTAGAAA	2160
GATCCCTGAC	TGCTTCTCAA	GATCCAGAAC	ATTCTTTGAC	AGAGTATATT	CACCATTTAG	2220
AAGTGATCCA	GCAAAGATTG	GGAGGGGTAC	TACCAGATTC	TACTTCAAAG	AAATCCTGCC	2280
ACCCGATGAT	TAAACAGTGA	ATAAAATGTC	ATGGCTCTTT	CCTGCGACAA	TTCTATTTGA	2340
GGAAAAGATT	TGTTTTTCCC	TTTTCCCAAG	GAAGCTCGTG	GGACAGCATG	GGCACTACTC	2400
TTCATGTGCG	GTGACACCAG	CCCCCAGATG	CCTTGAATTA	AGTGTCTCTA	CCTTTATGCA	2460
TGACTGCAAA	GCCAGCTGGA	GCATTTTCTA	TGGAGCCTCC	GTATGTTTTA	GGCCCATGAC	2520

CTTCGTGAGG TGATGGGCAC TCACTCCCAT GAGCCCTGGC TGTGTGCTGT TGTGTGCCTA	2580
TCGGCAGATC CATCCTTCCT GCCTCCAAGG AGGATACACA GAGAATGGCT TCCTGTTGTT	2640
TTGTTTATTT TCTTAACGTG TACAGATGGA AACTTCATTT AAAAATAAAA ACAAACAAY	2700
TCNAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2760
AAAA	2764

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Leu	Ile	Ser	Gly	Ser	Leu	Thr	Ser	Leu	Ser	Arg	Glu	Phe	Ser	Ala	1	5	10	15
Glu	Pro	Leu	Pro	Pro	Thr	Ala	Glu	Ser	Thr	Ala	Gly	Cys	Thr	Ser	Ala	20	25	30	
Glu	Gly	Ala	Ser	Pro	Arg	Ala	Gly	His	Phe	Gln	Gly	Leu	Leu	Ser	Gln	35	40	45	
Ser	Gly	Arg	Arg	Cys	Val	Gln	Arg	Thr	Pro	Leu	Pro	Arg	Ser	Thr	Glu	50	55	60	
Asn	Ala	Gly	Trp	Val	Cys	Gly	Ser	Gly	Pro	Val	Gly	Leu	Arg	Leu	Pro	65	70	75	80
Glu	Pro	Pro	Pro	Thr	Gly	Thr	Met	Thr	Arg	His	Ser	Trp	Lys	Cys	Leu	85	90	95	
Thr	Lys	Leu	Leu	Leu	Phe	Cys	Cys	Phe	Leu	Arg	Asp	Gly	Leu	Ala		100	105	110	
Leu	Ser	Ser	Arg	Leu	Glu	Cys	Asn	Gly	Thr	Val	Thr	Ala	His	Cys	Ser	115	120	125	
Leu	Glu	Leu	Val	Gly	Ser	Ser	His	Pro	Pro	Val	Ser	Ala	Ser	Pro	Val	130	135	140	
Pro	Gly	Thr	Val	Gly	Met	Ser	Thr	Ala	Pro	Gly	Ser	Cys	Ile	Ser	Val	145	150	155	160
Asp	Ser	Thr	Phe																

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CAGAAGGGAG GTAGTCGCCC TCCGTCGTGG CCTGGCGTGG ATTCCGAGCG TTGGTGTCTG	60
GCGGTTTCCG ACCGTTGGTG TCTGGCACGC GCCACCCCGA TGTACCAGGT AAAGCCCTAT	120
CACGGGGTCG GCGCCCCTCT CCGTGTGGAG CCCACCTGCA TGTACTGGCT CCCCAACATG	180
CACGGCAGGA GCGGCGGCCC AGCACTCGGC ACTGGCCACT TGCAGACAAG AAGACAAGAA	240
AATGATTTGA GGACAGCTTC AATCGCGGTG TGAAGAAGAA AGCAACAAAA CGACCACTGA	300
AAACAATGCC GGTGGCAAAA CATCCAAAGA AAGGGTCCCA AGCGGTACAT CGTCATAGCT	360
GGAAACAGTC AGAGCCACCA GCCAATGATC TTTTCAATGC TGCGAAAGCT GCCAAAAGTG	420
ACATGCAGTG TGGCCATGAG GTCTGCCGGA AGTGACTTGT TGGTGTTATC TCCTGAGTTA	480
AAATGTGAAG GGATTTTTTT TTTTCAGATT ACTGAGAGTC TTCTGTTACT AGTTTGTCTT	540
TCCTAGATCC AGACACGGGG ACTGCAGAGA AAGGCTGTGT GCATCCGCTG TCTACTCCAC	600
TGTCTCCTCT GCAGAGGCGG ATTTCCCTGA CTGAAGACCA TGTTCAGGC CCACAGCTGC	660
CTACAGAACC GTCCCAAAT ATGGCAAAGA AACCTATTCT GAGGGTCTCA CCATGTTGCC	720
CAGGCTGGTC TTGAACTCCT GGACTCATCC TAAAGTGCTG GCCTCTCATT CCCTGTCTGT	780
GCACACCTCA CGGCAAGGGC CAGCCTGTTT CCTCCCGGTC ACCTCCAAAT CTTGCTGCTT	840
TTAATTCAAC TCAGAGGCCT AGCCAGGGTT GAGTTCTCAC CCACCTGTGC CGCCCTGCCT	900
TGTTACCTGG AAGCACAGCC TTGGGGACTG AGCAGGCCCT CACTGTCACT TTAAGAAGGG	960
AATCAGCCAC TTTGTGCTCA CCACCTCTGG GGAAGGTGTG AGAGGAGAGA AGGAAGTGGC	1020
TGTTTGGCTG CTGACAACAT GAAGACTTCC TGCGATGAGA ACAGAGGCAC AGGTGCCGGC	1080
CCTGCAGCCC CCAGAACCCG GACTGGAGGG GGCCATGGGG CGCCGGACCC TGGCCCTGCC	1140
CTGGGTGCTG CTGACCCTGC GTGTCACTGC AGGGACCCCG GAGGTGTGAG TACAAGTTCTG	1200
GATGGAGGCC ACCGAGCTCT CGTCCTTCAC CATCCGTTGT GGGTTCCTGG AGTCTGGCTC	1260
CATCTCCCTG GTGACTGTGA GCTGGGGGGG CCCCGATGGT GCTGGGGGGA CCACGCTGGC	1320

TGTGTTGCAC	CCGGAACCTG	GCATCCAGCA	ATGGGCCCCCT	GCTCGCCAGG	CCCCTGGGA	1380
AACCCAGAGC	AGCGTCTCTC	TTGCCCTGGA	AGTCTCTGGG	GCCAGCAGCC	CCTGCACCAA	1440
CACCACCTTC	TGCTGCAAGT	TTGCGTCCTT	CCCTGAGGGC	TCCTGGGAGG	CCTCTGGGAG	1500
CCTCCCGCCC	AGCTCAGACC	CAGGGCTCTC	TGTCCCGCCG	ACTCCTGCCC	CCATTCTGCG	1560
GGCAGACCTG	GCCGGGATCT	TGGGGGTCTC	AGGAGTCCTT	CTCTTTGACT	GTGGCTACCT	1620
CCTTCATCTG	CTGTGCCGAC	AGAAGCACCG	CCCTGCCCCCT	AGGCTCCAGC	CATCCCACAC	1680
CAGCTCCTAG	GCACTGAGAG	CACGAGCATG	GGCACCCAGC	CAGGCCTCCC	AGGCTGCTCT	1740
CCACGTCCCT	TATGCCACTA	TCAACACCAG	CTGCTGCCCA	GCTACTTTGG	ACACAGCTCA	1800
CCCCCGACAG	GGGGCCGTCC	TGTCGTTTCC	TGCTGTGACT	AAGTCAGCAA	CACAGTTCCT	1860
CTGACATGGG	CCTTGGCTGT	GCTTCTTTGG	GGGTGAAGAG	ATTGGGGAGG	AAGTCTCCAC	1920
CCCTGGGAGG	CAGAAGCCAG	GCATAGCGCG	CTGGCTAGGA	CTCCAGTACC	GTGAAGGGAG	1980
GCAGTGAGAG	CAGACATCTG	TGTCTCATTC	CTGATCTCAA	GGGGAAAGCA	AGAACAAGGG	2040
AGGCTTCCTC	AGGATCTCAA	ACCTGCGGAA	GGAGGACCAG	TCTGTGTACT	TCTGCCAAGT	2100
CCAGCTGGAC	ATACAGATCA	GCCCTCAGGC	AGCCCCCTCA	CAGGACCCCT	CTCCTGCCTG	2160
GACAGCTCTG	CTGGTCTCCC	CGTCCCCTGG	AGAAGAACAA	GGCCATGGGT	CGGCCCCTGC	2220
TGCTGCCCCCT	GCTGCTCCTG	CTGCAGCCGC	CAGCATTTCT	GCAGCCTGGT	GGCTCCACAG	2280
GATCTGGTCC	AAGCTACCTT	TATGGGGTCA	CTCAACCAAA	ACACCTCTCA	GCCTCCATGG	2340
GTGGCTCTGT	GGAAATCCCC	TTCTCCTTCT	ATTACCCCTG	GGAGTTAGCC	ACAGCTCCCCG	2400
ACGTGAGAAT	ATCCTGGAGA	CGGGGCCACT	TCCACGGGCA	GTCCTTCTAC	AGCACAAGGC	2460
CGCCTTCCAT	TCACAAGGAT	TATGTGAACC	GGCTCTTTCT	GAACTGGACA	GAGGGTCAGG	2520
AGAGCGGCTT	CCTCAGGATC	TCAAACCTGC	GGAAGGAGGA	CCAGTCTGTG	TATTTCTGCC	2580
GAGTCGAGCT	GGACACCCGG	AGATCAGGGA	GGCAGCAGTT	GCAGTCCATC	AAGGGGACCA	2640
AACTCACCAT	CACCCAGGCT	GTCACAACCA	CCACCACCTG	GACGCCCAGC	AGCACAACCA	2700
CCATAGCCGG	CCTCAGGGTC	ACAGAAAGCA	AAGGGCACTC	AGAATCATGG	CACCTAAGTC	2760
TGGACACTGC	CATCAGGGTT	GCATTGGCTG	TCGCTGTGCT	CAAACTGTG	ATTTTGGGAC	2820
TGCTGTGCCT	CCTCCTGTGG	TGGAGGAGAA	GGAAAGGTAG	CAGGGCGCCA	AGCAGTGACT	2880
TCTGACCAAC	AGAGTGTGGG	GAGAAGGGAT	GTGTATTAGC	CCCGGAGGAC	GTGATGTGAG	2940
ACCCGCTTGT	GAGTCCTCCA	CACTCGTTCC	CCATTGGCAA	GATACATGGA	GAGCACCTG	3000

AGGACCTTTA AAAGGCAAAG CCGCAAGGCA GAAGGAGGCT GGGTCCCTGA ATCACCGACT 3060
GGAGGAGAGT TACCTACAAG AGCCTTCATC CAGGAGCATC CACACTGCAA TGATATAGGA 3120
WTGAGGTCTG AACTCCACTG AATTAAACCA CTGGCATTTC GGGGCTGTTC ATTATAGCAG 3180
TGCAAAGAGT TCCTTTATCC TCCCCAAGGA TGGAAAATAC AATTTATTTT GCTTACCATA 3240
CACCCCTTTT CTCTTCGTCC ACATTTTCCA ATCTGTATGG TGGCTGTCTT CTATGGCAGA 3300
AGGTTTTGGG GAATAAATAG CGTGAAATGC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360
AAAAAAA 3367

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Gly Arg Pro Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro
1 5 10 15
Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
20 25 30
Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
35 40 45
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
50 55 60
Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
65 70 75 80
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
85 90 95
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
100 105 110
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
115 120 125
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
130 135 140
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Thr
145 150 155 160

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
195 200 205

Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser Ser
210 215 220

Asp Phe
225

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGGAAGAGAT GGTGACTGAG GCAGAAGCTA ATAGGGAAGA TGATAGGAAA GAAATTTTAC	60
CCAAGGGAAT TAGATTTAGC AAGAGAGCGA AGGAAAGCTG AGAGGCCAAA AACATCTCTG	120
AGGAAAAC TG ACTCTGAGAG AGAAGAGGTG ACAAGGGCAA ATGCACTCAA GGATGAAGAT	180
GCTTTTAAAG AAGAGCAAAA ACTTAAAGCG GAAGAAGGGG AAACAGAGAC AGAAGTWAGA	240
GCTGAGGAAG AGACAAAAGC TCCCCCAAAT GAAATGGGAT CTGATGCTGA RAACGAASCA	300
CCTGTGGAGG CTTCTGAGTT GTCTGACAAT CCAGGGCTTC TAGGAGAARA TTCACTAAAA	360
GAGACAGTGG TTCCCATATT TGAAGCAACG CCTGGATTTG AAAAGTCGCT GGAAAACATA	420
ACAGCTCTGA GGAAAGAAGG AGGAGGGGAA AGACTGAGTG AAGCCAGAGA CACAGAGCAC	480
AAAGACAGAG AAGAGCTGTC CAGCAGGGAG AATAGGGCCC TGAAGGAAGG GCACCGCCAA	540
GATGGAGAGG GGGCCTTAGC AGCTCCTGAA GCTGAGCCAG CAGGAAAGGT GCAGGCCCCCT	600
GAGGGGCTGA TCCCAGCCAC AGGCCAGGCA GAGGAGCTAG CAGCCAAAGA TCACGACTCC	660
TGCGCAGGAC TGGAGGGGAG AGCTGAAGGG CAAGGAGGAG TGGATGTCGT GCTAAGGACC	720
CAGGAAGCTG TTGCTGAGGA AGATCCCATA WTGGCAGAAA AGTTCAGGGA GGAAGCGGTG	780
GATGAGGACC CAGAGGAGGA AGAGGACAAA GAGTGCAATC TGGAGACAGA AGCGATGCAG	840

GACAGGAACT CGGAAGGGGA CGGGGACATG GAAGGAGAAG GAAACACACA AAAGAATGAG 900
 GGCATGGGAG GAGGAAGGGT TGTGGCTGTG GAAGTTCTAC ACGGAGGTGG TGAAACGGCA 960
 GAAACAGCCG CAGAGGAGAG GGAGGTGTTG GCAGGTTTCGG AGACAGCCGA GGAGAAAACA 1020
 ATAGCAAATA AAGCCTCCTC CTTTTCAGAT GTTGCTGAGG AAGAAACCTG GCACCAACAG 1080
 GATGAGTTAG TAGGAAAAAC AGCAGCTGCA GGAAGGTGG TGGTAGAGGA ATTAGCACGG 1140
 AGTGGGGAGG AAGTGCCAGC AGCAGAGGAG ATGACAGTGA CATATACAAC AGAGGCTGGG 1200
 GTGGGCACTC CAGGAGCCCT GGAGCGGAAG ACCTCAGGGC TAGGACAGGA GCAAGAGGAA 1260
 GGGTCAGAGG GCCAGGAGGC AGCCACTGGG AGTGGCGATG GGAGGCAGGA GACAGGAGCA 1320
 GCTGAAAAAT TCCGATTAGG ATTATCACGG GAGGGAGAGA GGAATTGAG TCCGGAGAGT 1380
 CTACAGGCGA TGGCAACACT TCCAGTGAAG CCTGATTTCA CTGAAACCCG AGAGAAGCAA 1440
 CAGCATATGG TGCAAGGAGA AAGCGAGACT GCAGATGTTT CCCCCAACAA CATGCAGGTC 1500
 TAGGAGACTT GCTGGCAGAC GGATAATTTA AAGATGTCTT CTGAAGATGT AAAGAGTGGA 1560
 GAAAGATTCA CGCAAGCATC TCACCAGGAT TCTTGATTTT CTCTCTCTCC TCTTTAGTTG 1620
 CTGGTTGCGC TTGTCTGAGA TGATTCCCAA TCTGTCAGCC CTGGTCAGTA GCTCAGTAAG 1680
 CACCTTGAGA ATAGCTCAAG TAGATCTGTA GGACCCCTCT TAGAAGCAGT GGTTCCCTCAT 1740
 GGAGAACTT GTGAGGCTGT TACACATTCT ACACACCTAA CATTATTTTC AAACAAAAT 1800
 GATAATTTTC AGATGCTTGA CTTTACCAA AGATCACTGG AAGGCCAGT CCTAATGTTA 1860
 GGGGTTTGTT TAAAGTCCTT TTTATTTTAC AATACAGAGC CCCAGTCAAT TCCACAATCT 1920
 CAATTTTATA CATGGGAATT TTATTTAAAA ATCTGTGGTT TGGGGCTTTA ATGAATTGGC 1980
 CTGTGAAAAT GAGCTCTAAA TTTCTCCCA CGTACACTCA AACTCAAGA TTGCTCCAAA 2040
 TCTCTAAGTT CTTCCAGCAA AAGATTTCTT GGCATGTATA TTCACTTATA CTTAGAAATA 2100
 TTCATTCTTT TAATTTATGC CAGAATAACA AAGTGGAAT CTTATTTCAA AATGCTCTTT 2160
 GTTTTTTTGT GTGTGTTTCT GTAGTTCTGC TTTCTGGGGT AGACTAGTAA AATGGTAGCT 2220
 TCCAGCATTT TGTCCCTGGG GCCTTCTTTA TAGGGCCACT CAAATTTAAA TAAAGTAGT 2280
 AAATAATTTA GCTAAGTGGA ATAAGTATAA TAATTATAGT GGTAAGCATA GCACATCAGC 2340
 ATTATGCCAA CATTCTAGAC TCTTTAGTTG ATGTCATTAA ATGGAAAAGA AACTTGGAAT 2400
 AAATGAGTGT GCTGCTCACC TTCCAAGTT CTGTTATTTT AAACCTGTGA ACTAACCTTG 2460
 CAGTTCATTA TAAATCAACA GTAACAACCTG CATTCTAAAT TACTCCCTGA TATTATTTTC 2520

TAGTTGTGTA TCAGCCTGTC TCCTAGGGGT TTTCATTTCC CTGAAGACAT ACAAGTGCCC	2580
CAGAGCGCAT GTATATGTCT ACCATTTCTC TATATGAGAA GGTAACAAAAA ATTTCTTTAA	2640
GCAGTGATTT TCCAGCCAGA ATATACATTA GATTTTCATG GGACGCTTTT ATAAATGACT	2700
CAACCCTTTT CCCACCCCA GAGATTCAGA CTTAATTCGT TTTAGATGGA TCTACACATC	2760
AGTATATATA TATTTTAAAC TTTTCACTTG ATTCTTCTCT GTAGCCAAGG TTGAGAACCG	2820
CTGTTCTAAA TCATCATATA ATCCATGCTG GCCACATTAC ACTCAAGGTC CCTAGGGACC	2880
AGGCATATTA TCATAGTAGG TATCTTCCAT TTTAATGTGT AATGGAGCCA TTCAATGATC	2940
AAAAATACAC TGGACCAGAT AGTAGACTGG TCCCTTGATC AGAAGCATCA GCACATCAGC	3000
ATCACCTGGA AATTGTTCCC AGCCTTTGTC TCCTACCTAC TAAATTAGAA ACTCTTGGTG	3060
GGTTCCAGTA ATCCATAGCT TAACAAGCCC TGCAGTTAAT ACTGATGTAC ACTGATGTCC	3120
AAAAACTGCT GTCATGGACT ATTGATTGTA TTGAGGATTA GTCTCAGTTG GAAAGCCAAC	3180
TACAGAGGCA TTTTGAACCT TCTTTCTTTG CCTCTCTATG TCTCTCTGTC TTTTCTGTCT	3240
TTCTGATTTA TCTGTCTTTC TTTCTCTAGT AAATGGCACT CAATATAAAA GTGGTGGAGT	3300
CAATCTTAAA CTTATTTTAA TTATGATTGT ATTGATACAT GCACGAAGTC CCTCTGCCCT	3360
ACTCCCTATT CAAGGATATT ACTCACTGCA CATCATAAAT CTCCATCATC TGTCTTAAAG	3420
TTTTATGAGT AGATTTTCATC TACATTATAT TCAAGTTCAT TTATTACTGA GCTGTATTAC	3480
TGTGGAGCTC TAACAGTATT TGTTTCCTGA TTTCAAACCTC AATGCTACAG AGCACTTTGA	3540
ATACATCACA CCTTATAGGA AAGATAGTAA ATGTATTAAT CCCATTGAAA AATTAGTTTT	3600
GTACAATGTG CTAAATAGTA TTGCATTGGA TTACTTTTAT ATTTAACACA CTCCATCAAA	3660
ACATCCCATA ACATAATTTT ACAATCTGCA TGTGAATTTA ACTGTGAAAT TCAGTATTGT	3720
GATATTTTGA ATAAGTGAAT TCTTTCTCTG CAAATACTAT GTTGATAAAA TTACTTGTAT	3780
GTTCCCCTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3840
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGA	3899

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ile Gly Lys Lys Phe Tyr Pro Arg Glu Leu Asp Leu Ala Arg Glu
1 5 10 15

Arg Arg Lys Ala Glu Arg Pro Lys Thr Ser Leu Arg Lys Thr Asp Ser
20 25 30

Glu Arg Glu Glu Val Thr Arg Ala Asn Ala Leu Lys Asp Glu Asp Ala
35 40 45

Phe Lys Glu Glu Gln Lys Leu Lys Ala Glu Glu Gly Glu Thr Glu Thr
50 55 60

Glu Val Arg Ala Glu Glu Glu Thr Lys Ala Pro Pro Asn Glu Met Gly
65 70 75 80

Ser Asp Ala Glu Asn Glu Xaa Pro Val Glu Ala Ser Glu Leu Ser Asp
85 90 95

Asn Pro Gly Leu Leu Gly Glu Xaa Ser Leu Lys Glu Thr Val Val Pro
100 105 110

Ile Phe Glu Ala Thr Pro Gly Phe Glu Lys Ser Leu Glu Asn Ile Thr
115 120 125

Ala Leu Arg Lys Glu Gly Gly Gly Glu Arg Leu Ser Glu Ala Arg Asp
130 135 140

Thr Glu His Lys Asp Arg Glu Glu Leu Ser Ser Arg Glu Asn Arg Ala
145 150 155 160

Leu Lys Glu Gly His Arg Gln Asp Gly Glu Gly Ala Leu Ala Ala Pro
165 170 175

Glu Ala Glu Pro Ala Gly Lys Val Gln Ala Pro Glu Gly Leu Ile Pro
180 185 190

Ala Thr Gly Gln Ala Glu Glu Leu Ala Ala Lys Asp His Asp Ser Cys
195 200 205

Ala Gly Leu Glu Gly Arg Ala Glu Gly Gln Gly Gly Val Asp Val Val
210 215 220

Leu Arg Thr Gln Glu Ala Val Ala Glu Glu Asp Pro Ile Xaa Ala Glu
225 230 235 240

Lys Phe Arg Glu Glu Ala Val Asp Glu Asp Pro Glu Glu Glu Glu Asp
245 250 255

Lys Glu Cys Xaa Leu Glu Thr Glu Ala Met Gln Asp Arg Asn Ser Glu
260 265 270

Gly Asp Gly Asp Met Glu Gly Glu Gly Asn Thr Gln Lys Asn Glu Gly
275 280 285

Met Gly Gly Gly Arg Val Val Ala Val Glu Val Leu His Gly Gly Gly
 290 295 300
 Glu Thr Ala Glu Thr Ala Ala Glu Glu Arg Glu Val Leu Ala Gly Ser
 305 310 315 320
 Glu Thr Ala Glu Glu Lys Thr Ile Ala Asn Lys Ala Ser Ser Phe Ser
 325 330 335
 Asp Val Ala Glu Glu Glu Thr Trp His Gln Gln Asp Glu Leu Val Gly
 340 345 350
 Lys Thr Ala Ala Ala Gly Lys Val Val Val Glu Glu Leu Ala Arg Ser
 355 360 365
 Gly Glu Glu Val Pro Ala Ala Glu Glu Met Thr Val Thr Tyr Thr Thr
 370 375 380
 Glu Ala Gly Val Gly Thr Pro Gly Ala Leu Glu Arg Lys Thr Ser Gly
 385 390 395 400
 Leu Gly Gln Glu Gln Glu Glu Gly Ser Glu Gly Gln Glu Ala Ala Thr
 405 410 415
 Gly Ser Gly Asp Gly Arg Gln Glu Thr Gly Ala Ala Glu Lys Phe Arg
 420 425 430
 Leu Gly Leu Ser Arg Glu Gly Glu Arg Glu Leu Ser Pro Glu Ser Leu
 435 440 445
 Gln Ala Met Ala Thr Leu Pro Val Lys Pro Asp Phe Thr Glu Thr Arg
 450 455 460
 Glu Lys Gln Gln His Met Val Gln Gly Glu Ser Glu Thr Ala Asp Val
 465 470 475 480
 Ser Pro Asn Asn Met Gln Val
 485

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CATTGCTAGA CAGACTCTCT TGCTTGGATG GTACTCCACC ACTTTCTTGG CACATGAGAT 60
 GCAAGATTGC TCAGGGTGCA GCTAATGGCA TCAATTTTCT ACATGAAAAT CATCATATTC 120

ATAGAGATAT TAAAAGTGCA AATATCTTAC TGGATGAAGC TTTTACTGCT AAAATATCTG 180
 ACTTTGGCCT TGCACGGGCT TCTGAGAAGT TTTGCCCAGA CAGTCATGAC TAGCAGAATT 240
 GTGGGAACAA CAGCTTATAT GGCACCAGAA GCTTTGCGTG GAGAAATAAC ACCCAAATCT 300
 GATATTTACA GCTTTGGTGT GGTTTTACTA GAAATAATAA CTGGACTTCC AGCTGTGGAT 360
 GAACACCGTG AACCTCAGTT ATTGCTAGAT ATTAAAGAAG AAATTGAAGA TGAAGAAAAG 420
 ACATTGAAGA TTATATTGAT AAAAAGATGA ATGATGCTGA TTCCACTTCA GTTGAAGCTA 480
 TGT 483

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ala Ser Ile Phe Tyr Met Lys Ile Ile Ile Phe Ile Glu Ile Leu
 1 5 10 15
 Lys Val Gln Ile Ser Tyr Trp Met Lys Leu Leu Leu Leu Lys Tyr Leu
 20 25 30
 Thr Leu Ala Leu His Gly Leu Leu Arg Ser Phe Ala Gln Thr Val Met
 35 40 45
 Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met Ala Pro Glu Ala Leu
 50 55 60
 Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr Ser Phe Gly Val Val
 65 70 75 80
 Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val Asp Glu His Arg Glu
 85 90 95
 Pro Gln Leu Leu Leu Asp Ile Lys Glu Glu Ile Glu Asp Glu Glu Lys
 100 105 110
 Thr Leu Lys Ile Ile Leu Ile Lys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AATCTGAGTC AGCTTAGAAG ATANTCCAAG CTTCAGATGA TAACCACAGC CTGGGCTGAC	60
ACCTGGATTT CAGCTTTGCA TGATCCTCAG TATGAGAATC TATCTGTTCT GTGCTGGACT	120
TCTAATATAT AGAACTGTGA GATAATGGGT CACATTGGCT GGATGTGGTG GCTCATACCT	180
GTAAATCCCA GCACTTTGGG AGGCCGAGGC AGGCAGATCA CCTGAGGTCA GGAGTTCAAG	240
ACCGGCCTGG CCAGCATGGT GAAGCCCCGT CTTTACTAGA AATACAAAAA TTAGACGAGC	300
GTGGTGGTGG ACACCTGTGT TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG ACTGGCTGGA	360
ACCAGGGAGG TAGAGGTTGC AGTGAGCTGA GATCGTGCCA CTGCACTCCA GCCTGGGTGA	420
CAGAGTGAGA CTCCATCATA AATAAATAAA TAAATAAATG GGTACATTA AGCCTTTAAA	480
AAAAAAAAAA AAA	493

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2682 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GGTTCCCAAG AGAGTTTGCG ACGTGGTAAA GAAATAAGGC GAGTACACAA GCGAAGACTT	60
TCCAGCTCAG AGAGTGAAGA GAGCTATTTG TCCAAGAAGT CTGAAGATGA TGAGCTAGCT	120
AAAGAATCAA AGCGGTCAGT TCGAAAGCGG GGCCGAAGCA CAGACGAGTA TTCAGAAGCA	180
GATGAGGAGG AGGAGGAAGA RGAAGGCAAA CCATCCCGCA AACGGCTACA CCGGATTGAG	240
ACGGATGAGG ARGAGAGTTG TGACAATGCT CATGGAGATG CAAATCAGCC TGCCCGTGAC	300
AGCCAGCCTA GGGTCCTGCC CTCAGAACAA GAGAGCACCA AGAAGCCCTA CCGGATAGAA	360
AGTGATGAGG AAGAGGACTT TGAAAATGTA GGCAAAGTGG GGAGCCCATT GGAATATAGC	420
TTAGTGGACT TACCTTCAAC CAATGGACAG AGCCCTGGCA AAGCCATTGA GAACTTGATT	480

GGCAAGCCTA	CTGAGAAGTC	TCAGACCCCC	AAGGACAACA	GCACAGCCAG	TGCAAGCCTA	540
GCYTCCCAAT	GGGACAAGTG	GTGGGCAGGA	GGCAGGAGCA	CCAGAAGAGG	AGGAAGATGA	600
GCTTTTGAGA	GTGACTGACC	TTGTTGATTA	TGTCTGTAAC	AGTGAACAGT	TATAAGACTT	660
TTTTTCCATT	TTTGTGCTAA	TTTATTCCAC	GGTAGCTCTC	ACACCAGCGG	GCCAGTTATT	720
AAAAGCTGTT	TAATTTTTTC	TAGAAACTC	CACTACAGAA	TGACTTTTAG	AAGAAAAATT	780
TCAACAAATC	CTGAAGTCTT	TCTGTGAAGT	GACCAGTTCT	GAACCTTGAA	GATAAATAAT	840
TGCTGTAAAT	TCCTTTTGAT	TTTCTTTTTC	CAGGTTCATG	GTCCTTGGA	ATTCATTCA	900
TGGAAAAAAA	TCTTATTATA	ATAACAACAA	AGATTTGTAT	ATTTTTGACT	TTATATTTCC	960
TGAGCTCTCC	TGACTTTGTG	AAAAAGGGTG	ATGAAAATGC	ATTCCGAATC	TGTGAGGGCC	1020
CAAAACAGAA	TTTAGGGGTG	GGTGAAAGCA	CTTGTGCTTT	AGCTTTTTCA	TATTAAATAT	1080
ATATTATATT	TAAACATTCA	TGGCATAGAT	GATGATTTAC	AGACAATTTA	AAAGTTCAAG	1140
TCTGTACTGT	TACAGTTTGA	GAATTGTAGA	TAACATCATA	CATAAGTCAT	TTAGTAACAG	1200
CCTTTGTGAA	ATGAACCTGT	TTACTATTGG	AGATAACCAC	ACTTAATAAA	GAAGAGACAG	1260
TGAAAGTACC	ATCATAATTA	ACCTAAATTT	TTGTTATAGC	AGAGTTTCTT	GTTTAAAAAA	1320
AAAWAAAANG	CRKCYGMAAA	GCATTTGTAC	AGTAAAATGT	ATAATGAAGC	TTTGCCAACC	1380
AGACTGTGCT	AGCAACAAAT	TTTTTTAAAT	AAGCTTTATG	CAGTGGAAT	AAGGTGGCCT	1440
CAAATATATT	GTGTCTGATG	GAGAGTTATT	AGTGAAATGA	ATGTGGTCTT	TCTTAAGGCC	1500
TGGGTGGACT	GTAAACTTTG	CCAATAGTAT	AACCTTTGTC	TTCTGGCCAC	TTGATGTTTA	1560
AATATCTGAA	ATATCATTTT	GAAAAAATA	CATCTATATA	TAACATACAT	GAAGAGATGC	1620
TAAGCTGACA	GTGATATTTT	AGCACATTTG	AAGACTGGGA	AGAGATTTTC	AGGTGAATTT	1680
TAAGTGGTCT	ATTCTTGCCC	TTAGTATCTA	CTTCAAATTG	AAGTCTACAA	ACAAAGCAGT	1740
TCCTTTGGGA	GGTTTTTAGT	TTGAGTTTTA	GCGTGTGTGT	GTGTTTGTGT	GTGTGCGTGT	1800
GCGTGTGTGT	GTGTGTTGGA	ATTCCTATC	TGCCTGGATA	TATTAGCAGA	GTTTGAATGT	1860
AGTTTTGGCC	TTTGGCCATT	AGACTTCTAT	TAAAATTCAT	TAATAGTCAT	ACAACCAACA	1920
TAGAGTTGAA	TGAGAACTGC	CGATGTAATT	AATAGGCATG	ACATCCATTT	CAAACATCTC	1980
AACACTTTAA	AGAAAAGCCC	TTTGTTTCAA	GAAAAAAGGG	TTTGTAACATA	ACTAAATACC	2040
TAACATGTAA	TTGACACTAA	AATATGAACT	TTGTCTTATT	TAGTTTCTGT	TATAGCTGTA	2100
AAATTTACAG	CAGAGCCATA	ACATTGTACA	GAGTGTAGCA	CTTGTGATTA	AACCTAGCCT	2160
GTAAATCCT	GAAACCTTCA	ACCATTACTT	CTGTGAATAC	TTTAGCCCTG	GGATTTGGGT	2220

TTTTCTGTTC CGGTGTTGTG TCTGTTGCCG GCAATGGACA CACCATATCT GCTGCTGGCC 2280
 CAAGGAACGT CATTAATTTT TCTTTCCAAA TTAAGTATTA TGTGCTAGTC AGTGTATAGT 2340
 AAAGCACTTC TCTTTTTTAT TACTAAAAAG CTGGCATTAG ATTTGCATTA TAAATACCTC 2400
 TCTAGGAACT TTATACTCCT TTTCCTTCTT CAACAGGTAT TGCCCTTAAA TCTTATCTTT 2460
 TGGCCTTGAA AGTTTATAGC TATTGTTTTT CAGTTGTTCG TTGTTTGTGTT TTGTTTCACT 2520
 TTAGTTCTGT AGTACCTGCC CATTAATATT TTTGCTTTGA TTCTAGCAAT GTGTATGTAT 2580
 CTGTATAAAA AATAAAATAA TGAAAGCAAC CTAAAAATAG GATGCACCAA TTAAAAAAA 2640
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2682

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met	Glu	Lys	Asn	Leu	Ile	Ile	Ile	Thr	Thr	Lys	Ile	Cys	Ile	Phe	Leu
1				5					10				15		
Thr	Leu	Tyr	Phe	Leu	Ser	Ser	Pro	Asp	Phe	Val	Lys	Lys	Gly	Asp	Glu
			20					25					30		
Asn	Ala	Phe	Arg	Ile	Cys	Glu	Gly	Pro	Lys	Gln	Asn	Leu	Gly	Val	Gly
	35						40					45			
Glu	Ser	Thr	Cys	Ala	Leu	Ala	Phe	Ser	Tyr						
	50						55								

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGAGCGCC CGCGCCGCCG CTGCCTCTGT CCTCCGCGCG CTGCTCAGCT GAAGGCGCAC	60
AGGATTCAAT TACTGGACTT GTCAACTCTG CCAGTGTACG TGCCATTTCT CTTCCACTAT	120
GAGAGGACCG ATTGTATTGC ACATTGTCTT GGCTTTCTGT AGCCTTCTGC TTTTCAGCGT	180
TGCCACACAA TGTCTGGCCT TCCCCAAAAT AGAAAGGAGG AGGGAGATAG CACATGTTCA	240
TGCGGAAAAA GGGCAGTCCG ATAAGATGAA CACCGATGAC CTAGAAAATA GCTCTGTTAC	300
CTCAAAGCAG ACTCCCCAAC TGGTGGTCTC TGAAGATCCA ATGATGATGT CAGCAGTACC	360
ATCGGCAACA TCATTAAATA AAGCATTCTC GATTAACAAA GAAACCCAGC CTGGACAAGC	420
TGGGCTCATG CAAACAGAAC GCCCTGGTGT TTCCACACYT ACTGAGTCAG GTGTCCCCTC	480
AGCTGAAGAA GTATTTGGTT CCAGCCAGCC AGAGAGAATA TCTCCTGAAA GTGGACTTGC	540
CAAGGCCATG TTAACCATG CTATCACTGC GACTCCTTCT CTGACTGTTG ATGAAAAGGA	600
GGAACCTCCTT ACAAGCACTA ACTTTCAGCC CATTGTAGAA GAGATCACAG AAACCACAAA	660
AGGTTTTCTG AAGTATATGG ATAATCAATC ATTTGCAACT GAAAGTCAGG AAGGAGTTGG	720
TTTGGGACAT TCACCTTCAT CCTATGTGAA TACTAAGGAA ATGCTAACCA CCAATCCAAA	780
GACTGAGAAA TTTGAAGCAG ACACAGACCA CAGGACAAC TCTTTTCCTG GTGCTGAGTC	840
CACAGCAGGC AGTGAGCCTG GAAGCCTCAC CCCTGATAAG GAGAAGCCTT CGCAGATGAC	900
AGCTGATAAC ACCCAGGCTG CTGCCACCAA GCAACCACTC GAAACTTCCG AGTACACCCT	960
GAGTGTGAG CCAGAACTG ATAGTCTGCT GGGAGCCCCA GAAGTCACAG TGAGTGTCAG	1020
CACAGCTGTT CCAGCTGCCT CTGCCTTAAG TGATGAGTGG GATGACACCA AATTAGAGAG	1080
TGTAAGCCGG ATAAGGACCC CCAAGCTTGG AGACAATGAA GAGACTCAGG TGAGAACGGA	1140
GATGTCTCAG ACAGCACAAG TAAGCCATGA GGGTATGGAA GGAGGCCAGC CTTGGACAGA	1200
GGCTGCACAG GTGGCTCTGG GGCTGCCTGA AGGGGAAACA CACACGGGCA CAGCCCTGCT	1260
AATAGCGCAT GGAATGAGA GATCACCTGC TTTCCTGAT CAAAGTTCCT TTACCCCCAC	1320
AAGTCTGATG GAAGACATGA AAGTTTCCAT TGTGAACTTG CTCCAAAGTA CGGGAGACTT	1380
CACGGAATCC ACCAAGGAAA ACGATGCCCT GTTTTTCTTA GAAACCACTG TTTCTGTCTC	1440
TGTATATGAG TCTGAGGCAG ACCAACTGTT GGGAAATACA ATGAAAGACA TCATCACTCA	1500
AGAGATGACA ACAGCTGTTC AAGAGCCAGA TGCCACTTTA TCCATGGTGA CACAAGAGCA	1560
GGTTGCTACC CTCGAGCTTA TCAGAGACAG TGGCAAGACT GAGGAAGAAA AGGAGGACCC	1620
CTCTCCTGTG TCTGACGTTT CTGGTGTAC TCAGCTGTCA AGAAGATGGG AGCCTCTGGC	1680
CACTACAATT TCAACTACAG TCGTCCCTTT GTCTTTTGAA GTTACTCCCA CTGTGGAAGA	1740

ACAAATGGAC ACAGTCACAG GGCCAAATGA GGAGTTCACA CCAGTTCCTGG GATCTCCAGT 1800
 GACACCTCCT GGAATAATGG TGGGGGAACC CAGCATTTCC CCTGCACTTC CTGCTTTGGA 1860
 GGCATCCTCT GAGAGAAGAA CTGTTGTTCC ATCTATTACT CGTGTTAATA CAGCTGCCCTC 1920
 ATATGGCCTG GACCAACTTG AATCTGAAGA GGGACAAGAA GATGAGGATG AAGAGGATGA 1980
 AGAAGATGAA GATGAAGAAG AGGAAGATGA GGAAGAAGAT GAGGAAGATA AAGATGCAGA 2040
 CTCGCTGGAT GAGGGCTTGG ATGGTGACAC TGAGCTGCCA GGTTTTACCC TCCCTGGTAT 2100
 CACATCCCAG GAACCAGGCT TAGAGGAGGG AAACATGGAC CTGTTGGAGG GAGCTACCTA 2160
 CCAGGTGCCA GATGCCYTCG AGTGGAACA GCAGAATCAA GGCCTGGTGA GAAGCTGGAT 2220
 GGAAAAATTM AAAGACAAGG CTGGTTACAT GTCTGGGATG CTGGTGCCTG TAGGGGTTGG 2280
 GATAGCTGGA GCCTTGTTCA TCTTGGGAGC CCTCTACAGC ATTAAGGTTA TGAATCGCCG 2340
 AAGGAGAAAT GGCTTCAAAA GGCATAAAAG AAAGCAGAGA GAATTCAACA GCATGCAAGA 2400
 TCGAGTAATG CTCTTAGCCG ACAGCTCTGA AGATGAATTT TGAATTGGAC TGGGTTTTAA 2460
 TTGGGATATT CAACGATGCT ACTATTCTAA TTTTATTTT GGAGCAGAAA AAAAAAAAAA 2520
 AA 2522

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met	Arg	Gly	Pro	Ile	Val	Leu	His	Ile	Cys	Leu	Ala	Phe	Cys	Ser	Leu
1					5				10					15	
Leu	Leu	Phe	Ser	Val	Ala	Thr	Gln	Cys	Leu	Ala	Phe	Pro	Lys	Ile	Glu
			20					25					30		
Arg	Arg	Arg	Glu	Ile	Ala	His	Val	His	Ala	Glu	Lys	Gly	Gln	Ser	Asp
		35					40					45			
Lys	Met	Asn	Thr	Asp	Asp	Leu	Glu	Asn	Ser	Ser	Val	Thr	Ser	Lys	Gln
	50					55					60				
Thr	Pro	Gln	Leu	Val	Val	Ser	Glu	Asp	Pro	Met	Met	Met	Ser	Ala	Val
65						70				75				80	

Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr
 85 90 95
 Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser
 100 105 110
 Thr Xaa Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser
 115 120 125
 Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met
 130 135 140
 Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys
 145 150 155 160
 Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile
 165 170 175
 Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe
 180 185 190
 Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser
 195 200 205
 Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys
 210 215 220
 Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu
 225 230 235 240
 Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys
 245 250 255
 Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln
 260 265 270
 Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp
 275 280 285
 Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val
 290 295 300
 Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu
 305 310 315 320
 Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr
 325 330 335
 Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly
 340 345 350
 Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly
 355 360 365
 Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His
 370 375 380

Gly Asn Glu Arg Ser Pro Ala Phe Thr Asp Gln Ser Ser Phe Thr Pro
 385 390 395 400
 Thr Ser Leu Met Glu Asp Met Lys Val Ser Ile Val Asn Leu Leu Gln
 405 410 415
 Ser Thr Gly Asp Phe Thr Glu Ser Thr Lys Glu Asn Asp Ala Leu Phe
 420 425 430
 Phe Leu Glu Thr Thr Val Ser Val Ser Val Tyr Glu Ser Glu Ala Asp
 435 440 445
 Gln Leu Leu Gly Asn Thr Met Lys Asp Ile Ile Thr Gln Glu Met Thr
 450 455 460
 Thr Ala Val Gln Glu Pro Asp Ala Thr Leu Ser Met Val Thr Gln Glu
 465 470 475 480
 Gln Val Ala Thr Leu Glu Leu Ile Arg Asp Ser Gly Lys Thr Glu Glu
 485 490 495
 Glu Lys Glu Asp Pro Ser Pro Val Ser Asp Val Pro Gly Val Thr Gln
 500 505 510
 Leu Ser Arg Arg Trp Glu Pro Leu Ala Thr Thr Ile Ser Thr Thr Val
 515 520 525
 Val Pro Leu Ser Phe Glu Val Thr Pro Thr Val Glu Glu Gln Met Asp
 530 535 540
 Thr Val Thr Gly Pro Asn Glu Glu Phe Thr Pro Val Leu Gly Ser Pro
 545 550 555 560
 Val Thr Pro Pro Gly Ile Met Val Gly Glu Pro Ser Ile Ser Pro Ala
 565 570 575
 Leu Pro Ala Leu Glu Ala Ser Ser Glu Arg Arg Thr Val Val Pro Ser
 580 585 590
 Ile Thr Arg Val Asn Thr Ala Ala Ser Tyr Gly Leu Asp Gln Leu Glu
 595 600 605
 Ser Glu Glu Gly Gln Glu Asp Glu Asp Glu Glu Asp Glu Glu Asp Glu
 610 615 620
 Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Glu Glu Asp Lys Asp Ala
 625 630 635 640
 Asp Ser Leu Asp Glu Gly Leu Asp Gly Asp Thr Glu Leu Pro Gly Phe
 645 650 655
 Thr Leu Pro Gly Ile Thr Ser Gln Glu Pro Gly Leu Glu Glu Gly Asn
 660 665 670
 Met Asp Leu Leu Glu Gly Ala Thr Tyr Gln Val Pro Asp Ala Xaa Glu
 675 680 685

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Xaa
 690 695 700
 Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val
 705 710 715 720
 Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys
 725 730 735
 Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys
 740 745 750
 Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp
 755 760 765
 Ser Ser Glu Asp Glu Phe
 770

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2002 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCAGCCCGG TACCTGAAGT CCTTCAGAAAG TGCACGCCGG GACCAGGATT CCGGGAGGCC	60
GACTCCTCCC TGCCCCACGA ATGCCGGGAA TTGTGGTCTC CGCCGGACGC GAGTTGTGAG	120
ACGGCCCAAG GGGCCGCGGG GTATGCTGGG ACCGCTAGCC CTTCCGGCGC GCCTCAGGAC	180
TTCGGGTCCC CTCACCCCGG GCGGATGCCC AAAGACTCCG CCTTCCCAAG AGCCCCTGCG	240
GCCGGGCGCG AAAATGGCGG CGGCGGCGAC GGCCGGGCGC TCCTGAAGCA GCAGTTATGG	300
AGCTTCCCTC AGGGCCGGGG CCGGAGCGGC TCTTTGACTC GCACCGGCTT CCGGGTGACT	360
GCTTCCTACT GCTCGTGCTG CTGCTCTACG CGCCAGTCGG GTTCTGCCTC CTCGTCCTGC	420
GCCTGTTTCT CGGGATCCAC GTCTTCCTGG TCAGCTGCGC GCTGCCAGAC AGCGTCCTTC	480
GCAGATTTCGT AGTGCGGACC ATGTGTGCGG TGCTAGGGCT CGTGGCCCGG CAGGAGGACT	540
CCGGACTCCG GGATCACAGT GTCAGGGTCC TCATTTCCAA CCATGTGACA CCTTTCGACC	600
ACAACATAGT CAATTTGCTT ACCACCTGTA GCACCGTGAG TGAGAGCGAG GCCGAGAGCG	660
CCACGGGGCG GTTCCCTGGG GCCCAGCTGA AGGCCCCCCT GTCCCCACTC GCGTTCCCCA	720
TGGAGGATAC TGAGCCTTAC CCCTAACCCC GATCCTCTAC CCAACATGTC AGTTTTTTTT	780

TTCATTTTCC TCAATATTTT TCTTCTTGCT TTCTCTTCTC CTGGTTCCCA GCCTCTACTC	840
AATAGTCCCC CCAGCTTTGT GTGCTGGTCT CGGGGCTTCA TGGAGATGAA TGGGCGGGGG	900
GAGTTGGTGG AGTCACTCAA GAGATTCTGT GCTTCCACGA GGCTTCCCCC CACTCCTCTG	960
CTGCTATTCC CTGAGGAAGA GGCCACCAAT GGCCGGGAGG GGCTCCTGCG CTTCAGAGTT	1020
TGACAGTTGC CTGTTATAAG GCAGGTGTGA GCTGCTGACT AGGCTGGCTG GATTCCCATC	1080
CTACTTTCTC CTTCTCTTTC TAGTTCCTGG CCATTTTCTA TCCAAGATGT GGTACAACCT	1140
CTTACCCTGC AAGTTCAGAG ACCCCTGGTC TCTGTGACGG TGTCAGATGC CTCCTGGGTC	1200
TCAGAACTGC TGTGGTCACT TTTCGTCCCT TTCACGGTGT ATCAAGTGGC TTCGTCTGT	1260
TCATCGCCAA CTAGGGGAAG CGAATGAGGA GTTTGCACTC CGTGTACAAC AGCTGGTGGC	1320
CAAGGAATTG GGCCAGACAG GGACACGGCT CACTCCAGCT GACAAAGCAG AGCACATGAA	1380
GCGACAAAGA CACCCAGAT TGCGCCCCCA GTCAGCCCAG TCTTCTTTCC CTCCCTCCCC	1440
TGGTCCTTCT CCTGATGTGC AACTGGCAAC TCTGGCTCAG AGAGTCAAGG AAGTTTTGCC	1500
CCATGTGCCA TTTGGTGTCA TCCAGAGAGA CCTGGCCAAG ACTGGCTGTG TAGACTTGAC	1560
TATCACTAAT CTGCTTGAGG GGGCCGTAGC TTTCATGCCT GAAGACATCA CCAAGGGAAC	1620
TCAGTCCCTA CCCACAGCCT CTGCCTCCAA GTTTCCCAGC TCTGGCCCCG TGACCCCTCA	1680
GCCAACAGCC CTAACATTTG CCAAGTCTTC CTGGGCCCCG CAGGAGAGCC TGCAGGAGCG	1740
CAAGCAAGCA CTATATGAAT ACGCAAGAAG GAGATTCACA GAGAGACGAG CCCAGGAGGC	1800
TGACTGAGCT CAAAGGAACA GGATGGCACC CAGAGCCGCA GGACGGAGAC TGGGGGCAGC	1860
CCTCACCCAA CTCACAACAG GCTGGATGGG TGGGTGGTAA AAAGGGAAGG ATGAGGCTCC	1920
CCCAATGTCA CATTAAATTC ATGGTTTTCA TTCAAGGVAA AAAAAAAAAA AAAAAAAAAA	1980
AAAAAAAAAA AAAAAAAAAA AA	2002

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met	Pro	Pro	Gly	Ser	Gln	Asn	Cys	Cys	Gly	His	Phe	Ser	Ser	Leu	Ser	1	5	10	15
Arg	Cys	Ile	Lys	Trp	Leu	Arg	Pro	Val	His	Arg	Gln	Leu	Gly	Glu	Ala	20	25	30	
Asn	Glu	Glu	Phe	Ala	Leu	Arg	Val	Gln	Gln	Leu	Val	Ala	Lys	Glu	Leu	35	40	45	
Gly	Gln	Thr	Gly	Thr	Arg	Leu	Thr	Pro	Ala	Asp	Lys	Ala	Glu	His	Met	50	55	60	
Lys	Arg	Gln	Arg	His	Pro	Arg	Leu	Arg	Pro	Gln	Ser	Ala	Gln	Ser	Ser	65	70	75	80
Phe	Pro	Pro	Ser	Pro	Gly	Pro	Ser	Pro	Asp	Val	Gln	Leu	Ala	Thr	Leu	85	90	95	
Ala	Gln	Arg	Val	Lys	Glu	Val	Leu	Pro	His	Val	Pro	Phe	Gly	Val	Ile	100	105	110	
Gln	Arg	Asp	Leu	Ala	Lys	Thr	Gly	Cys	Val	Asp	Leu	Thr	Ile	Thr	Asn	115	120	125	
Leu	Leu	Glu	Gly	Ala	Val	Ala	Phe	Met	Pro	Glu	Asp	Ile	Thr	Lys	Gly	130	135	140	
Thr	Gln	Ser	Leu	Pro	Thr	Ala	Ser	Ala	Ser	Lys	Phe	Pro	Ser	Ser	Gly	145	150	155	160
Pro	Val	Thr	Pro	Gln	Pro	Thr	Ala	Leu	Thr	Phe	Ala	Lys	Ser	Ser	Trp	165	170	175	
Ala	Arg	Gln	Glu	Ser	Leu	Gln	Glu	Arg	Lys	Gln	Ala	Leu	Tyr	Glu	Tyr	180	185	190	
Ala	Arg	Arg	Arg	Phe	Thr	Glu	Arg	Arg	Ala	Gln	Glu	Ala	Asp	195	200	205			

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CAATTGGGCC GCGAGTTGTG GTTTAAACCA GGAGTGC GCC GCGTCCGTTC ACCGCGGCCT	60
CAGATGAATG CGGCTGT TAA GACCTGCAAT AATCCAGAAT GGCTACTCTG ATCTATGTTG	120
ATAAGGAAAA TGGAGAACCA GGCACCCGTG TGGTTGCTAA GGATGGGCTG AAGCTGGGGT	180

CTGGACCTTC AATCAAAGCC TTAGATGGGA GATCTCAAGT TTCAACACCA CGTTTTGGCA	240
AAACGTTCTGA TGCCCCACCA GCCTTACCTA AAGCTACTAG AAAGGCTTTG GGAAGTGTCA	300
ACAGAGCTAC AGAAAAGTCT GTAAAGACCA AGGGACCCCT CAAACAAAAA CAGCCAAGCT	360
TTTCTGCCAA AAAGATGACT GAGAAGACTG TTAAAGCAAA AAGCTCTGTT CCTGCCTCAG	420
ATGATGCCTA TCCAGAAATA GAAAAATTCT TTCCCTTCAA TCCTCTAGAC TTTGAGAGTT	480
TTGACCTGCC TGAAGAGCAC CAGATTGCGC ACCTCCCCTT GAGTGGAGTG CCTCTCWTGA	540
TCCTTGACGA GGAGAGAGAG CTTGAAAAGC TGTTTCAGCT GGGCCCCCCT TCACCTGTGA	600
AGATGCCCTC TCCACCATGG GAATCCAATC TGTTGCAGTC TCCTTCAAGC ATTCTGTCGA	660
CCCTGGATGT TGAATTGCCA CCTGTTTGCT GTGACATAGA TATTTAAATT TCTTAGTGCT	720
TCAGAGTTTG TGTGTATTTG TATTAATAAA GCATTCTTTA ACAGAAAAAA AAAAAAAAAA	780
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met	Ala	Thr	Leu	Ile	Tyr	Val	Asp	Lys	Glu	Asn	Gly	Glu	Pro	Gly	Thr
1			5					10					15		
Arg	Val	Val	Ala	Lys	Asp	Gly	Leu	Lys	Leu	Gly	Ser	Gly	Pro	Ser	Ile
			20					25					30		
Lys	Ala	Leu	Asp	Gly	Arg	Ser	Gln	Val	Ser	Thr	Pro	Arg	Phe	Gly	Lys
			35				40					45			
Thr	Phe	Asp	Ala	Pro	Pro	Ala	Leu	Pro	Lys	Ala	Thr	Arg	Lys	Ala	Leu
	50					55				60					
Gly	Thr	Val	Asn	Arg	Ala	Thr	Glu	Lys	Ser	Val	Lys	Thr	Lys	Gly	Pro
65				70					75					80	
Leu	Lys	Gln	Lys	Gln	Pro	Ser	Phe	Ser	Ala	Lys	Lys	Met	Thr	Glu	Lys
			85					90						95	
Thr	Val	Lys	Ala	Lys	Ser	Ser	Val	Pro	Ala	Ser	Asp	Asp	Ala	Tyr	Pro

100	105	110
Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe		
115	120	125
Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val		
130	135	140
Pro Leu		
145		

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNTCCTGCCTC AGCTGCCTCT CTGTGTAA

29

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CNCACTGCCCT CTTTCTCCCA TAGGTACT

29

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAATAAGCAT GATGCTCTAC AAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TNGGTGCCATG ATTCTGAGTG CCCTTTGC

29

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNATATGTCAC TGTCATCTCC TCTGCTGC

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANAAGCTTCAT CCAGTAAGAT ATTTGCAC

29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ANTTCAGAACT GGTCACCTCA CAGAAAGA

29

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNATTCACATA GGATGAAGGT GAATGTCC

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANTAGAGGCTG GGAACCAGGA GAAGAGAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TNTTGCAGGTC TTAACAGCCG CATTTCATC

29

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
1 5 10 15
Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
 20 25 30
Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
 35 40 45
Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
 50 55 60
Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
65 70 75 80
Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
 85 90 95
Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
 100 105 110
Thr

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Gln Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg
1 5 10 15
Gly Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys
 20 25 30
Arg Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe
 35 40 45
Pro Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ser Ser Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu
1 5 10 15

Gln Val Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp
 20 25 30

Val Ser Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln
 35 40 45

Val

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CAGGTGGTCC TCCACCTGCC TTGGCTTCCT AAAGTGCTGG GATTACAGGC ATGAGTCACT 60
CTGCTGGCCT ATGTTCTGTT TTTGTTTTTG TTTTGTGTTT GAGACAGAGT TTCACTCTTG 120
TTGCCCAGGC TGGAGTGCAA TGGCATAATC TCGGCTCACT GCAGCCTCTG CCTCCCAGGT 180
TCAAGTGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAT GTGCCACCTC 240
ACCTGGCTAA TTTTGTATTT TTAGTAGAGA TGGGGTTTCT CCATGTTAGT CAGGCTGGTC 300
TTGAACTCCT GACCTCAGGT GATCTGCCCT CCTCAGCCTC CTAAAGTGCT GGGATTACAG 360
GTGTGAGCCA CTGTGCCAG CCTTGTTTTT TGTGTTTTTG TTTTGTGTTT TTTTTTTGAC 420
AGTAGCCATC CTAATAGATA CTAAGTGGTA TCTCATTGTG GTTTTGATTG CATGCGTTCT 480
TTTTGGCTTG TTTTTTGAGA CAAGGTCTCA CTCCATCACC CAGACTGGAG CGCAGTGGTG 540
TGATCACGGC TCGTTGCAAC CTGACCCTCT TGAGCTCAGG TGATCCTCCC ACTTCACCCT 600
CCCGAGTATC TTGGAGTACA GGTGTGTGCC TGGCTGATTT TTCGTATTTT TTGTAGAGAT 660

GGGGTTTCAC	CGTGTGCTC	AGGCTGCTCT	CAAACCTGCTG	GGCTCAAACG	ATCCTCCTGC	720
CTTGGCCTCC	CAAAGTGCTG	GGGTTACAAG	CATGAACCAT	TATGCCCGGC	CTGCATGCAC	780
TCTTACACAC	GTTTTATCTG	TTACATATCC	CAAGATGTGT	AGTTCTTTGG	GAAGCAGGAA	840
GAAATGGGGG	TAACATTGAG	AAGTTAAGGA	AAACTGGTAT	AAATTATTGG	CAGCAGCTCC	900
TGATTATAGG	TTTTGAGGCC	TGAGTCCATG	GGCAGAGTCC	CTCTCCTGCA	GTTTCATGAGA	960
TTTGTACCCT	CCAGTGACAG	TACTGGGAAG	GAGGGAATGC	TACGTTCCAA	CTCTTAGTCT	1020
TCACTTAATT	TTATGACTCA	AAATTCCAGC	TAGATATATA	GGTTACTTTT	ACTGTTGGAT	1080
CACTCTGGCC	CACGAATGTA	TCCTGCTAAC	TTGATGTGTG	CTCTAACTAC	CTCCTAAGTT	1140
TGGTGACAGT	CGGCAGAGTT	TGTGAACCAT	GTGATTCCCA	ACTTAAGTTA	CTAACATTTT	1200
TTTTTTTTTT	TTTTGAGACA	GGATCTTGCT	CTGTCACCCA	GGCTGGAGTG	CAGTGGTACG	1260
ATCTCAGCTC	ACTGTAGCCT	TAACCCACCC	AGGCTTATGT	GCTCCTCCCA	CCTCAGCCTC	1320
CCGAGTAGTT	GGAACATAG	GTGCATACCA	CCATGCCTGG	CTAATTTTGT	TATTTTTTGT	1380
AGAGGCAGGG	TTTTGCCCTG	TTGCCCAGGC	TGGTCTTGAA	CTCCTGAGCT	CAAGCAATCC	1440
TCCCACCTCA	GCCTCCCAA	GGGTTGGGAT	TACAGGTGTG	AGCCACTGCA	CCCGGCCAAG	1500
TTACTAACAT	TTTAAGTCTA	AAGTAAAAGA	TTGCTTCTGT	ATGTTCTCCC	CCAGGTGTGT	1560
AGGTCCATCC	TGGGAAGGCC	ATCAGACACA	CCTAGTCCAT	GGGTGACACC	CAGCCAGTTT	1620
TTAATGCCAG	TTCCTCTGGC	AGTTTTTAAT	TTAGGCACTC	GGAAGTGAAA	CCCGGACATT	1680
CACTGGAAAT	GACTTTAGGA	CAAGACCTGC	TGGCCATGAG	CTGAGAAATG	TCTTACTCTC	1740
TTGCAGGGAG	AATGCTGTTG	AAAGACTTGA	TTCATTAATA	CAAGCGACTC	ACGTTGCAAT	1800
GAGAGGCAAC	TCCGATTACG	CTGATCTTAG	TGATGGCTGG	CTCGAAATAA	TACGTGTAGA	1860
TGCCCCTGAT	CCAGGTGCAG	ACCCGCTGGC	TAGCAGTGTG	AACGGCATGT	GCCTGGATAT	1920
TCCTGCTCAC	CTGAGCATCC	GCATCCTCAT	CTCGGATGCT	GGCGCGGTGG	AAGGGATTAC	1980
TCAGCAGGAG	ATACTCGGTG	TAGAGACAAG	GTTCTCCTCA	GTGAACTGGC	AGTACCAGTG	2040
TGGGCTTACC	TGTGAGCACA	AGGCCGACCT	TCTCCCTATC	AGTGCATCCG	TCCAGTTTAT	2100
TAAAATTCCT	GCACAGTTAC	CCCACCCCT	GACAAGATTC	CAGATCAATT	ATACAGAGTA	2160
TGACTGCAAC	AGAAATGAGG	TGTGTTGGCC	GCAGCTTCTA	TATCCATGGA	CTCAGTATTA	2220
TCAAGGGGAG	CTGCATTCTC	AGTGTGTTGC	TAAGGGCTTA	CTGTTGCTGT	TGTTCCCTCAC	2280
ATTGGCCTTG	TTCCTCAGCA	ACCCCTGGAC	CAGAATATGC	AAAGCCTATA	GTTAGACAAC	2340

CACCTGGCTT TTATTTTTTT GAGATGGAGT TTTGCTCTTG TTACCCAGGC TGGAGTGCAG 2400
 TGCACAATCT CGGCTCACTG CAATCTCTGC CTCCCAAGCA ATCCTCCCAC CTCAGCCTCT 2460
 GGTGTAGCTG GGACCACAGA TGCTCCACCA TGCCTGGCTG TATTTTTGGT AAAGATGGGG 2520
 TTTCGCCTTG TTGCCCAGGG TGGTCTGTAA CTCCTGAGCT CAGATGATCT GCCCACCTCG 2580
 GCCTCCCAAA GTGCTGGGAT CACAGACGTG AGCCACTGCG TCCGGTCCAT CTGACTTCTC 2640
 AAAGACTTTA GACCTTGACT TCAGTGATTT GTTGTAGTCT TGTATGCTTC TCTATAAAAT 2700
 TTTAATAAAT GAAATGTCTT ATTTTGTAG AAAATTTTAA AAAAAAAAAA AAAA 2754

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Arg Gly Asn Ser Asp Tyr Ala Asp Leu Ser Asp Gly Trp Leu Glu
 1 5 10 15
 Ile Ile Arg Val Asp Ala Pro Asp Pro Gly Ala Asp Pro Leu Ala Ser
 20 25 30
 Ser Val Asn Gly Met Cys Leu Asp Ile Pro Ala His Leu Ser Ile Arg
 35 40 45
 Ile Leu Ile Ser Asp Ala Gly Ala Val Glu Gly Ile Thr Gln Gln Glu
 50 55 60
 Ile Leu Gly Val Glu Thr Arg Phe Ser Ser Val Asn Trp Gln Tyr Gln
 65 70 75 80
 Cys Gly Leu Thr Cys Glu His Lys Ala Asp Leu Leu Pro Ile Ser Ala
 85 90 95
 Ser Val Gln Phe Ile Lys Ile Pro Ala Gln Leu Pro His Pro Leu Thr
 100 105 110
 Arg Phe Gln Ile Asn Tyr Thr Glu Tyr Asp Cys Asn Arg Asn Glu Val
 115 120 125
 Cys Trp Pro Gln Leu Leu Tyr Pro Trp Thr Gln Tyr Tyr Gln Gly Glu
 130 135 140
 Leu His Ser Gln Cys Val Ala Lys Gly Leu Leu Leu Leu Phe Leu

145 150 155 160

Thr Leu Ala Leu Phe Leu Ser Asn Pro Trp Thr Arg Ile Cys Lys Ala

 165 170 175

Tyr Ser

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TAGGCCATGA AGGCCGGTTT TTCATAAAAT AGGAATGAGG ACAAATGTTG CTCTTCATCC	60
TACCAGCTGT TTGTTCTTTG GTAGGGGATC ATGAGTGGAA AAACAAAGGC AAGAAGGGCT	120
GCCATGTTTT TTAGACGTTG CTCTGAAGAC GCCAGCGGTA GCGCCAGTGG CAATGCTTTG	180
TTATCAGAGG ACGAAAATCC TGATGCGAAT GGGGTAAGTC GATCATGGAA GATTATTCTA	240
AGTACAATGC TTAACTGAC TTTTCTTCTT GTAGGACTCC TAAATCATCA GTGGCTTAAA	300
GAAACAGATG TTCCTCAGAA ATCCAGACAA TTATATGCCA TAATTGCAGA ATATGGTTCA	360
AGGCTTTATA AATATCAGGC CAGACTTCGT ATGCCTAAAG AGCAACTGGA ACTTTTAAAG	420
AAGGAAAGCC AGAATCTGGA AAACAATTTT CGTCAAATTC TATTTTGTAT CGAACAAATA	480
GATGTCCTGA AGGCATTGCT AAGAGATATG AAGGATGGTA TGGACAATAA TCACAAGTGG	540
AACACCCATG GAGACCCTGT GGAGGACCCG GACCACACAG AGGAAGTGTC AAAGTTGGTC	600
AATTATGTAC TTAAAAAGTT GAGAGAAGAC CAAGTCGAGA TGGCTGATTA TGCCCTGAAG	660
TCGGCCGGAG CCTCCATCAT TGAAGCTGGG ACCTCAGAAA GTTATAAAAA TAATAAAGCA	720
AAATTGTACT GGCATGGGAT AGGTTTCCTA AATCATGAAA TGCCTCCAGA TATTATTCTT	780
CAGCCGGATG TCTACCCTGG AAAGTGCTGG GCTTTTCCAG GTTCCCAGGG TCATACCCTA	840
ATCAAGCTTT ACAAAGATCA TACCAACTGC TGTTACCATG GAGCACATCT CAGAGAAGGT	900
GTCTCCGTCA GGAAACATCT CCAGTGCACC CAAGGAATTT TCTGTCTATG GCATCACAAA	960
AAAATGTGAA GGAGAAGAAA TTTTCCTAGG TCAGTTTATA TATAACAAA CAGGAACCAC	1020
CGTTCAAACA TTTGAACTCC AGCATGCAGT TTCTGAATAT TTATTATGTG TGAAACTTAA	1080

TATCTTTAGC AACTGGGGAC ACCCGAAGTA TACTTGTTTA TATCGATTCA GGGTCCATGG 1140
CACACCAGGC AAGCACATCT AGAAGAGTTG GTACAGAAGG CCATGCCACA TGTCCAGAAT 1200
ATTCAAGAAT GCTTATTCTC TTAGATGATA CCGCACCCAT AGGAATTGAG AATTGGGAGT 1260
GGGAAGAAAA CCTCAAAGTG GTTCATACTT GCCTGTAAAA AGTAAATGCA TTTTACTAAT 1320
AAAAAATAT GGAAGTAAAT TAAAAA AAA 1363

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ser	Gly	Lys	Thr	Lys	Ala	Arg	Arg	Ala	Ala	Met	Phe	Phe	Arg	Arg	1	5	10	15
Cys	Ser	Glu	Asp	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Asn	Ala	Leu	Leu	Ser	20	25	30	
Glu	Asp	Glu	Asn	Pro	Asp	Ala	Asn	Gly	Val	Thr	Arg	Ser	Trp	Lys	Ile	35	40	45	
Ile	Leu	Ser	Thr	Met	Leu	Thr	Leu	Thr	Phe	Leu	Leu	Val	Gly	Leu	Leu	50	55	60	
Asn	His	Gln	Trp	Leu	Lys	Glu	Thr	Asp	Val	Pro	Gln	Lys	Ser	Arg	Gln	65	70	75	80
Leu	Tyr	Ala	Ile	Ile	Ala	Glu	Tyr	Gly	Ser	Arg	Leu	Tyr	Lys	Tyr	Gln	85	90	95	
Ala	Arg	Leu	Arg	Met	Pro	Lys	Glu	Gln	Leu	Glu	Leu	Leu	Lys	Lys	Glu	100	105	110	
Ser	Gln	Asn	Leu	Glu	Asn	Asn	Phe	Arg	Gln	Ile	Leu	Phe	Leu	Ile	Glu	115	120	125	
Gln	Ile	Asp	Val	Leu	Lys	Ala	Leu	Leu	Arg	Asp	Met	Lys	Asp	Gly	Met	130	135	140	
Asp	Asn	Asn	His	Asn	Trp	Asn	Thr	His	Gly	Asp	Pro	Val	Glu	Asp	Pro	145	150	155	160
Asp	His	Thr	Glu	Glu	Val	Ser	Asn	Leu	Val	Asn	Tyr	Val	Leu	Lys	Lys				

165	170	175
Leu Arg Glu Asp Gln Val Glu Met Ala Asp Tyr Ala Leu Lys Ser Ala		
180	185	190
Gly Ala Ser Ile Ile Glu Ala Gly Thr Ser Glu Ser Tyr Lys Asn Asn		
195	200	205
Lys Ala Lys Leu Tyr Trp His Gly Ile Gly Phe Leu Asn His Glu Met		
210	215	220
Pro Pro Asp Ile Ile Leu Gln Pro Asp Val Tyr Pro Gly Lys Cys Trp		
225	230	235
Ala Phe Pro Gly Ser Gln Gly His Thr Leu Ile Lys Leu Tyr Lys Asp		
245	250	255
His Thr Asn Cys Cys Tyr His Gly Ala His Leu Arg Glu Gly Val Ser		
260	265	270
Val Arg Lys His Leu Gln Cys Thr Gln Gly Ile Phe Cys Leu Trp His		
275	280	285
His Lys Lys Met		
290		

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GGGCTGCATT TCCAGCAGGA GCTGCGAGCA CAGTGCTGGC TCACAACAAG ATGCTCAAGG	60
TGTCAGCCGT ACTGTGTGTG TGTGCAGCCG CTTGGTGCAG TCAGTCTCTC GCAGCTGCCG	120
CGGCGGTGGC TGCAGCCGGG GGGCGGTCGG ACGGCGGTAA TTTTCTGGAT GATAACAAT	180
GGCTCACCAC AATCTCTCAG TATGACAAGG AAGTCGGACA GTGGAACAAA TTCCGAGACG	240
AAGTAGAGGA TGATTATTTT CGCACTTGGA GTCCAGGAAA ACCCTTCGAT CAGGCTTTAG	300
ATCCAGCTAA GGATCCATGC TTAAAGATGA AATGTAGTCG CCATAAAGTA TGCATTGCTC	360
AAGATTCTCA GACTGCAGTC TGCATTAGTC ACCGGAGGCT TACACACAGG ATGAAAGAAG	420
CAGGAGTAGA CCATAGGCAG TGGAGGGGTC CCATATTATC CACCTGCAAG CAGTGCCAG	480
TGGTCTATCC CAGCCCTGTT TGTGGTTCAG ATGGTCATAC CTACTCTTTT CAGTGCAAAC	540

TAGAATATCA	GGCATGTGTC	TTAGGAAAAC	AGATCTCAGT	CAAATGTGAA	GGACATTGCC	600
CATGTCCTTC	AGATAAGCCC	ACCAGTACAA	GCAGAAATGT	TAAGAGAGCA	TGCAGTGACC	660
TGGAGTTCAG	GGAAGTGGCA	AACAGATTGC	GGGACTGGTT	CAAGGCCCTT	CATGAAAGTG	720
GAAGTCAAAA	CAAGAAGACA	AAAACATTGC	TGAGGCCTGA	GAGAAGCAGA	TTCGATACCA	780
GCATCTTGCC	AATTTGCAAG	GACTCACTTG	GCTGGATGTT	TAACAGACTT	GATACAAACT	840
ATGACCTGCT	ATTGGACCAG	TCAGAGCTCA	GAAGCATTTA	CCTTGATAAG	AATGAACAGT	900
GTACCAAGGC	ATTCTTCAAT	TCTTGTGACA	CATACAAGGA	CAGTTTAATA	TCTAATAATG	960
AGTGGTGCTA	CTGCTTCCAG	AGACAGCAAG	ACCCACCTTG	CCAGACTGAG	CTCAGCAATA	1020
TTCAGAAGCG	GCAAGGGGTT	AAGAAGCTCC	TAGGACAGTA	TATCCCCCTG	TGTGATGAAG	1080
ATGGTTACTA	CAAGCCAACA	CAATGTCATG	GCAGTGTTGG	ACAGTGCTGG	TGTGTTGACA	1140
GATATGGAAA	TGAAGTCATG	GGATCCAGAA	TAAATGGTGT	TGCAGATTGT	GCTATAGATT	1200
TTGAGATCTC	CGGAGATTTT	GCTAGTGGCG	ATTTTCATGA	ATGGACTGAT	GATGAGGATG	1260
ATGAAGACGA	TATTATGAAT	GATGAAGATG	AAATTGAAGA	TGATGATGAA	GATGAAGGGG	1320
ATGATGATGA	TGGTGGTGAT	GACCATGATG	TATACATTTA	ATTGATGACA	GTTGAAATCA	1380
ATAAATTCTA	CATTTCTAAT	ATTTACAAAA	ATGATAGCCT	ATTTAAAATT	ATCTTCTTCC	1440
CCAATAACAA	AATGATTCTA	AACCTCACAT	ATATTTTGTA	TAATTATTTG	AAAAATTGCA	1500
GCTAAAGTTA	TAGAACTTTA	TGTTTAAATA	AGAATCATTT	GCTTTGAGTT	TTTATATTCC	1560
TTACACAAAA	AGAAAATACA	TATGCAGTCT	AGTCAGACAA	AATAAAGTTT	TGAAGTGCTA	1620
CTATAATAAG	TTTTTCACGA	GAACAACTT	TGTAAATCTT	CCATAAGCAA	AATGACAGCT	1680
AGTGCTTGGG	ATCGTACATG	TTAATTTTCT	GAAAGATAAT	TCTAAGTGAA	ATTTAAAATA	1740
AATAAATTTT	TAATGACCTG	GGTCTTAAGG	ATTTAGGAAA	AATATGCATG	CTTTAATTGC	1800
ATTTCCAAAG	TAGCATCTTG	CTAGACCTAG	TTGAGTCAGG	ATAACAGAGA	GATACCACAT	1860
GGCAAGAAAA	ACAAAGTGAC	AATTGTAGAG	TCCTCAATTG	TGTTTACATT	AATAGTGGTG	1920
TTTTTACCTA	TGAAATTATT	CTGGATCTAA	TAGGACATTT	TACAAAATGG	CAAGTATGGA	1980
AAACCATGGA	TTCTGAAAGT	TAAAAATTTA	GTTGTTCTCC	CCAATGTGTA	TTTAAATTTG	2040
GATGGCAGTC	TCATGCAGAT	TTTTTAAAAG	ATTCTTTAAT	AACATGATTT	GTTTGCCTTT	2100
CTAGATTTCT	TTATCTTTCT	GACCAGCAAC	TTAGGGAGCA	GAATTTAAAT	TAGGAAGACA	2160
AAGGGAAAGA	TTCATTTAAA	CCATATTTTT	ACAAAGTTTG	TCATTTGCCC	CAAGGTCAAA	2220

TTTTAAATTC TTAATTTTCA TTTTATTTC CATTTTAGGT AAAAGTTTGC ATTTAATCTT 2280
 AGAATTATGT TATTTTGTG AGTAGTGTGG AAACCTTAGAG AACCTTATTGT ATGGTGCCCTT 2340
 GCAAAAATAG AGATAGAAAG ATTTTAGCAT GCATACCAAT ATAGTATATT ACGCAATATA 2400
 TAAGCACACC TAATTAACAG ATTAATATCA GTAAAGGTAT TGCTGCTGGA ATGAAGAAAA 2460
 TGGGATACGT TTGTTTCTTT TTTTCTATTG TWACATAATT GCCATGTGGA CTTGTTTATG 2520
 ATTATTGTGT AGAGTAGCAT TTAAGATTTA ACTGTAGCAA AAATTACTTT AACCGCTGTA 2580
 TTTAAGTTAG CATGTTAATT AATTGTGTAG ACATTTTGGC ACACCATCAC TTTTAACTAT 2640
 ATCATACCAA TGGTTTGTG CCCATAATAA AAATGGAAAA ACCTGTTGAA TGTTACGTAT 2700
 TGGTATCTTT AATTCAACA GTGGGTAAAC TGGTTTCCCA GTATACAATT CATTGAAAGC 2760
 AAAATTGATT AATTATTTCC ATTTAATTTA TACACACTCA ATACAAAATT TAATGTTGAC 2820
 TTTACGTAAT AAAGTATAAT GCATTTTCTT TTTTACTGTT TATGTATAGT TTACAAAATA 2880
 AAGAATCTTG TAACCAAAAA AAAAAAAAAA A 2911

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp	Cys
1				5				10						15	
Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly	Gly	Arg	
			20					25					30		
Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu	Thr	Thr	Ile
		35					40						45		
Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys	Phe	Arg	Asp	Glu
		50					55				60				
Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	Gly	Lys	Pro	Phe	Asp
65					70					75				80	
Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	Leu	Lys	Met	Lys	Cys	Ser
				85					90					95	

Arg His Lys Val Cys Ile Ala Gln Asp Ser Gln Thr Ala Val Cys Ile
 100 105 110
 Ser His Arg Arg Leu Thr His Arg Met Lys Glu Ala Gly Val Asp His
 115 120 125
 Arg Gln Trp Arg Gly Pro Ile Leu Ser Thr Cys Lys Gln Cys Pro Val
 130 135 140
 Val Tyr Pro Ser Pro Val Cys Gly Ser Asp Gly His Thr Tyr Ser Phe
 145 150 155 160
 Gln Cys Lys Leu Glu Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser
 165 170 175
 Val Lys Cys Glu Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser
 180 185 190
 Thr Ser Arg Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu
 195 200 205
 Val Ala Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly
 210 215 220
 Ser Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg
 225 230 235 240
 Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp Met
 245 250 255
 Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln Ser Glu
 260 265 270
 Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr Lys Ala Phe
 275 280 285
 Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile Ser Asn Asn Glu
 290 295 300
 Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro Pro Cys Gln Thr Glu
 305 310 315 320
 Leu Ser Asn Ile Gln Lys Arg Gln Gly Val Lys Lys Leu Leu Gly Gln
 325 330 335
 Tyr Ile Pro Leu Cys Asp Glu Asp Gly Tyr Tyr Lys Pro Thr Gln Cys
 340 345 350
 His Gly Ser Val Gly Gln Cys Trp Cys Val Asp Arg Tyr Gly Asn Glu
 355 360 365
 Val Met Gly Ser Arg Ile Asn Gly Val Ala Asp Cys Ala Ile Asp Phe
 370 375 380
 Glu Ile Ser Gly Asp Phe Ala Ser Gly Asp Phe His Glu Trp Thr Asp
 385 390 395 400

Asp Glu Asp Asp Glu Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu
405 410 415

Asp Asp Asp Glu Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His
420 425 430

Asp Val Tyr Ile
435

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGATTCTGAAG TTTAAGAAAC TGCATTTTAA AGTGCCCAAA GTTTCATTTT CTTCTACCAA	60
AACTCCTAAA GATAGTTTAG TCCCAGGTGC AAAGTCTAGC ATAGGTCTTT CCACGATTCC	120
TTTATCATCT TCAGAATGCT CAAGTTTTGA ATTACAACAG GTTTCGGCTT GTTCAGAGCC	180
ATCCATGCAG ATGCCTAAGG TGGGTTTTGC TGGGTTTCCA TCATCCCGGC TTGATCTCAC	240
TGGTCCCTCAC TTTGAATCTT CTATTCTCTC TCCCTGTGAG GATGTTACAC TTACAAAATA	300
CCAGGTGACT GTTCCCCAGA GCTGCCTTGG CCCCTGAGCT TGCTCTGGAA ATTCCTTCTG	360
GGTCTCAGGC TGATATTCCT CTTCCCAAGA CAGAGTGCTC CACTGAMCTG CAGCCTCCAG	420
ARGGAGTTCC AACATCTCAA GCTGAGAGTC ACTCTGGCCC ACTGAATTCC ATGATTCCTG	480
TTTCTCTTGG TCAGGTGTCT TTTCTAAAT TCTATAAACC AAAGTTTGTG TTTTCAGTCC	540
CCCAAATGGC AGTTCCTGAG GGAGACCTAC ATGCAGCAGT GGGTGCCCCA GTCATGTYTC	600
YTCTTAGCCC TTGGAGAAAG AGTGCAGTGC CCCTTGCCAA GCACCCAGYT GCCATCCCCA	660
GGCACCTGTG TGTCCCAGGG CCCAGAAGAG CTTGTGGCCT CTTGCAGAC ATCAGTAGTG	720
GCCCYTGGAG AAGCCCCTTC TGAAGATGCT GACCACGAAG GGAAAGGGAG TCCCTTGAAA	780
ATGCCTAAGA TTAAGCTTCC ATCATTTAGG TGGTCCCCGA AGAAGGAAAC AGGGCCAAAG	840
GTGGACCCAG AATGCAGCGT GGAGGACTCA AAACCTCAGCC TGGTTTTAGA CAAGGATGAA	900
GTGGCCCCGC AGTCTGCCAT CCACATGGAT CTGCCTCCTG AGAGGGATGG AGAGAAGGGG	960
AGGAGCACAA AGCCTGGCTT TGCCATGCCA AAACCTGCAC TTCCCAAAT GAAGGCTTCT	1020

AAGAGTGGGG	TCAGCCTGCC	ACAGAGAGAC	GTGGATCCTT	CCCTTTCTAG	TGCCACAGCA	1080
GGGGGTAGCT	TTCAAGACAC	AGAAAAGGCC	AGCAGTGACG	GTGGTAGGGG	AGGACTTGGT	1140
GCAACAGCAA	GTGCCACAGG	AAGTGAGGGT	GTGAACCTCC	ACCGGCCACA	GGTCCACATT	1200
CCCAGTTTGG	GCTTTGCCAA	ACCTGATCTC	AGATCCTCCA	AGGCCAAGGT	GGAGGTGAGC	1260
CAGCCTGAAG	CTGACCTGCC	TCTTCCCAAA	CATGATCTGT	CTACCGAAGG	TGACAGCAGA	1320
GGATGTGGGC	TCGAGGATGT	CCCAGTGAGC	CAGCCTTGTG	GGGAGGGGAT	AGCCCCCACA	1380
CCTGAAGATC	CCCTCCAGCC	ATCCTGTAGA	AAACCAGATG	CTGAAGTCCT	CACAGTGGA	1440
AGCCCAGAGG	AGGAAGCCAT	GACCAAGGAC	TCGCAGGAAA	GCTGGTTTAA	AATGCCCAAG	1500
TTCCGCATGC	CCAGCCTTAG	GCGCTCTTTC	AGGGACAGAG	GCGGGGCTGG	AAAGCTGGAA	1560
GTGGCTCAGA	CACAGGCACC	GGCAGCAACA	GGGGGTGAAG	CAGCAGCTAA	AGTCAAAGAG	1620
TTCCTTGTTT	CTGGGTCAAA	CGTGGAGGCA	GCTATGTCCC	TACAGCTCCC	AGAGGCAGAT	1680
GCAGAAGTGA	CAGCTTCTGA	GAGCAAATCA	TCCACAGATA	TTCTAAGGTG	TGATCTTGAC	1740
AGCACAGGCT	TGAAGTGCA	CCTTTCCACT	GCTGGGATGA	CTGGGGATGA	GCTTTCCACT	1800
TCTGAGGTCA	GGATCCATCC	ATCCAAAGGA	CCTCTCCCTT	TTCAGATGCC	TGGCATGAGG	1860
CTTCCAGAAA	CCCAGGTTCT	TCCAGGAGAA	ATAGATGAGA	CTCCTCTTTC	CAAGCCAGGA	1920
CATGACCTTG	CCAGCATGGA	GGATAAAACA	GAGAAATGGT	CTTCCCAGCC	TGAAGGTCCA	1980
CTTAAATTGA	AAGCTTCAAG	TACTGATATG	CCATCCAGAA	TTTCTGTGGT	TAATGTGGAT	2040
CAACTGTGGG	AAGATTCTGT	CCTAACTGTC	AAATTCCCCA	AATTAATGGT	ACCAAGGTTC	2100
TCCTTCGCTG	CCCCCAGCTC	AGAGGATGAT	GTGTTTCATC	CCACTGTGAG	GGAAGTGCAG	2160
TGTCCAGAGG	CCAATATTGA	TACAGCCCTT	TGTAAGGAAA	GTCCGGGGCT	CTGGGGAGCC	2220
AGCATCCTGA	AGGCAGGTGC	TGGGGTCCCT	GGGGAGCAGC	CTGTGGACCT	TAACCTGCCT	2280
TTGGAAGCTC	CCCCAATTTC	AAAGGTCAGA	GTGCATATTC	AGGGTGCTCA	GGTTGAAAGT	2340
CAAGAGGTCA	CTATACACAG	CATAGTGACA	CCAGAGTTTG	TAGATCTCTC	AGTACCCAGG	2400
ACTTTTTCCA	CTCAGATTGT	GCGGGAATCA	GAGATCCCCA	CGTCAGAGAT	TCAAACACCT	2460
TCGTACGGAT	TTTCCTTATT	AAAAGTGAAA	ATCCCAGAGC	CCCACACGCA	GGCTAGAGTG	2520
TACACAACAA	TGACTCAACA	CTCTAGGACT	CAGGAGGGCA	CAGAAGAGGC	TCCCATACAA	2580
GCCACCCCAG	GAGTAGACTC	CATTTCTGGA	GATCTCCAGC	CTGACACTGG	AGAACCATTT	2640
GAGATGATCT	CTTCCAGCGT	CAATGTACTG	GGACAGCAAA	CACTCACATT	TGAAGTTCCT	2700

TCTGGCCACC AGCTTGCAGA CAGCTGTTCA GATGAGGAGC CAGCAGAAAT TCTTGAGTTT	2760
CCCCCTGATG ATAGCCAAGA GGCAACCACA CCACTGGCAG ATGAAGGCAG GGCTCCAAAA	2820
GACAAACCAG AAAGTAAAAA ATCTGGTCTG CTCTGGTTTT GGCTTCCAAA CATTGGGTTT	2880
TCCTCTTCTG TTGATGAGAC AGGTGTTGAT TCCAAAAATG ACGTCCAGAG ATCTGCTCCC	2940
ATTCAAACAC AGCCTGAGGC ACGACCAGAG GCAGAACTGC CTAAAAACA GGAGAAGGCA	3000
GGCTGGTTCC GATTTCCCAA ATTAGGGTTC TCCTCATCTC CTACCAAGAA AAGCAAAAGC	3060
ACCGAAGATG GGGCAGAGCT GGAAGAACAA AACTTCAAG AAGAAACAAT CACGTTTTTC	3120
GATGCCCCGAG AAAGTTTCTC CCCTGAAGAG AAGGAAGAGG GTGAACTGAT CGGGCCTGTG	3180
GGCACTGGGC TGGACTCCAG AGTGATGGTG ACATCCGCGG CAAGAACAGA GTTAATCCTG	3240
CCCGAGCAGG ACAGAAAAGC TGACGATGAA AGCAAAGGGT CAGGCCTGGG ACCAAATGAA	3300
GGCTGAGAGG TATGGCTCAT CGGTACAAGA GAGATGCAAA AAATAAGTT GGAAAGTAAA	3360
GGCTACACAC ACATATGGAG CACCCCATCC CACAGCACAT TACATCCACC TCACTTCACA	3420
GAACGGAGAA CAGAGCAGAA ATGACCAGAA CACCTTTGTC ACCATCACAC AGCCCTCCTA	3480
AAATGGAACC AAAGCTTCCC AGCTCCCTCA AAGCTTTGGA TGCAAAGAAG GCACCCTGAC	3540
TTCCACAAGA CACCAGAATT CACACGGTAC TCAGAGGCAC TGCTGGGGAA GTTTGTTGGT	3600
CTTTATTAGA TAAATTTCCTA GAGACCTGTC CATAATACCC AACAGAACAT GACTGTTTCT	3660
TTGAGGAAAG GGTATAATG TCTGTGGTGT ACAAGTCGTT TTTGGTATAA CTTCTTTCCT	3720
GCTGCTGCTG CTTCCCGGCA AACATAGTTT TCCTATTTCA GGCAGAGTGC GGTATATTCC	3780
AGGAAACACT GTTTCCTACT CACTTAGCTT ACTTCTTTGT TGAATGCCTC ACTAATGGCA	3840
AGTTTCAAGA TGTTTTGGGT GACAATGCAC ACATGCTGGG CAAAAGGGTG ATGGCCAGTG	3900
GCTGGCAGCT GGGCCAGCAG AAGCTAGGAC ATCTGTGAGT TGTCATTCTC ATCTATCCAT	3960
GTCCACTGGC CTGCCAGCAT CCGCCAGTGC CTTGCCAGTG TGCACGGTCC CAACTGTGG	4020
CCCCTGAGTC CCCTAATGTA CACGCTGCAG CCAGAATGCA GATGGAGCTG GCTTGGCTGT	4080
TCCCTGGATG GGCAATAAAG AAAGTGCTGC ATCCCCAAAAA AAAAAAAAAA	4130

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Gln	Gln	Trp	Val	Pro	Gln	Ser	Cys	Xaa	Xaa	Leu	Ala	Leu	Gly	Glu	
1				5					10					15		
Arg	Val	Gln	Cys	Pro	Leu	Pro	Ser	Thr	Gln	Leu	Pro	Ser	Pro	Gly	Thr	
			20					25					30			
Cys	Val	Ser	Gln	Gly	Pro	Glu	Glu	Leu	Val	Ala	Ser	Leu	Gln	Thr	Ser	
			35				40					45				
Val	Val	Ala	Xaa	Gly	Glu	Ala	Pro	Ser	Glu	Asp	Ala	Asp	His	Glu	Gly	
	50					55					60					
Lys	Gly	Ser	Pro	Leu	Lys	Met	Pro	Lys	Ile	Lys	Leu	Pro	Ser	Phe	Arg	
65				70						75					80	
Trp	Ser	Pro	Lys	Lys	Glu	Thr	Gly	Pro	Lys	Val	Asp	Pro	Glu	Cys	Ser	
				85					90					95		
Val	Glu	Asp	Ser	Lys	Leu	Ser	Leu	Val	Leu	Asp	Lys	Asp	Glu	Val	Ala	
			100					105					110			
Pro	Gln	Ser	Ala	Ile	His	Met	Asp	Leu	Pro	Pro	Glu	Arg	Asp	Gly	Glu	
			115				120					125				
Lys	Gly	Arg	Ser	Thr	Lys	Pro	Gly	Phe	Ala	Met	Pro	Lys	Leu	Ala	Leu	
	130					135					140					
Pro	Lys	Met	Lys	Ala	Ser	Lys	Ser	Gly	Val	Ser	Leu	Pro	Gln	Arg	Asp	
145					150					155					160	
Val	Asp	Pro	Ser	Leu	Ser	Ser	Ala	Thr	Ala	Gly	Gly	Ser	Phe	Gln	Asp	
				165					170					175		
Thr	Glu	Lys	Ala	Ser	Ser	Asp	Gly	Gly	Arg	Gly	Gly	Leu	Gly	Ala	Thr	
			180					185					190			
Ala	Ser	Ala	Thr	Gly	Ser	Glu	Gly	Val	Asn	Leu	His	Arg	Pro	Gln	Val	
			195				200					205				
His	Ile	Pro	Ser	Leu	Gly	Phe	Ala	Lys	Pro	Asp	Leu	Arg	Ser	Ser	Lys	
	210					215					220					
Ala	Lys	Val	Glu	Val	Ser	Gln	Pro	Glu	Ala	Asp	Leu	Pro	Leu	Pro	Lys	
225					230					235					240	
His	Asp	Leu	Ser	Thr	Glu	Gly	Asp	Ser	Arg	Gly	Cys	Gly	Leu	Glu	Asp	
				245					250					255		
Val	Pro	Val	Ser	Gln	Pro	Cys	Gly	Glu	Gly	Ile	Ala	Pro	Thr	Pro	Glu	
				260				265					270			

Asp Pro Leu Gln Pro Ser Cys Arg Lys Pro Asp Ala Glu Val Leu Thr
 275 280 285
 Val Glu Ser Pro Glu Glu Glu Ala Met Thr Lys Asp Ser Gln Glu Ser
 290 295 300
 Trp Phe Lys Met Pro Lys Phe Arg Met Pro Ser Leu Arg Arg Ser Phe
 305 310 315 320
 Arg Asp Arg Gly Gly Ala Gly Lys Leu Glu Val Ala Gln Thr Gln Ala
 325 330 335
 Pro Ala Ala Thr Gly Gly Glu Ala Ala Ala Lys Val Lys Glu Phe Leu
 340 345 350
 Val Ser Gly Ser Asn Val Glu Ala Ala Met Ser Leu Gln Leu Pro Glu
 355 360 365
 Ala Asp Ala Glu Val Thr Ala Ser Glu Ser Lys Ser Ser Thr Asp Ile
 370 375 380
 Leu Arg Cys Asp Leu Asp Ser Thr Gly Leu Lys Leu His Leu Ser Thr
 385 390 395 400
 Ala Gly Met Thr Gly Asp Glu Leu Ser Thr Ser Glu Val Arg Ile His
 405 410 415
 Pro Ser Lys Gly Pro Leu Pro Phe Gln Met Pro Gly Met Arg Leu Pro
 420 425 430
 Glu Thr Gln Val Leu Pro Gly Glu Ile Asp Glu Thr Pro Leu Ser Lys
 435 440 445
 Pro Gly His Asp Leu Ala Ser Met Glu Asp Lys Thr Glu Lys Trp Ser
 450 455 460
 Ser Gln Pro Glu Gly Pro Leu Lys Leu Lys Ala Ser Ser Thr Asp Met
 465 470 475 480
 Pro Ser Gln Ile Ser Val Val Asn Val Asp Gln Leu Trp Glu Asp Ser
 485 490 495
 Val Leu Thr Val Lys Phe Pro Lys Leu Met Val Pro Arg Phe Ser Phe
 500 505 510
 Ala Ala Pro Ser Ser Glu Asp Asp Val Phe Ile Pro Thr Val Arg Glu
 515 520 525
 Val Gln Cys Pro Glu Ala Asn Ile Asp Thr Ala Leu Cys Lys Glu Ser
 530 535 540
 Pro Gly Leu Trp Gly Ala Ser Ile Leu Lys Ala Gly Ala Gly Val Pro
 545 550 555 560
 Gly Glu Gln Pro Val Asp Leu Asn Leu Pro Leu Glu Ala Pro Pro Ile
 565 570 575

Ser Lys Val Arg Val His Ile Gln Gly Ala Gln Val Glu Ser Gln Glu
 580 585 590
 Val Thr Ile His Ser Ile Val Thr Pro Glu Phe Val Asp Leu Ser Val
 595 600 605
 Pro Arg Thr Phe Ser Thr Gln Ile Val Arg Glu Ser Glu Ile Pro Thr
 610 615 620
 Ser Glu Ile Gln Thr Pro Ser Tyr Gly Phe Ser Leu Leu Lys Val Lys
 625 630 635 640
 Ile Pro Glu Pro His Thr Gln Ala Arg Val Tyr Thr Thr Met Thr Gln
 645 650 655
 His Ser Arg Thr Gln Glu Gly Thr Glu Glu Ala Pro Ile Gln Ala Thr
 660 665 670
 Pro Gly Val Asp Ser Ile Ser Gly Asp Leu Gln Pro Asp Thr Gly Glu
 675 680 685
 Pro Phe Glu Met Ile Ser Ser Ser Val Asn Val Leu Gly Gln Gln Thr
 690 695 700
 Leu Thr Phe Glu Val Pro Ser Gly His Gln Leu Ala Asp Ser Cys Ser
 705 710 715 720
 Asp Glu Glu Pro Ala Glu Ile Leu Glu Phe Pro Pro Asp Asp Ser Gln
 725 730 735
 Glu Ala Thr Thr Pro Leu Ala Asp Glu Gly Arg Ala Pro Lys Asp Lys
 740 745 750
 Pro Glu Ser Lys Lys Ser Gly Leu Leu Trp Phe Trp Leu Pro Asn Ile
 755 760 765
 Gly Phe Ser Ser Ser Val Asp Glu Thr Gly Val Asp Ser Lys Asn Asp
 770 775 780
 Val Gln Arg Ser Ala Pro Ile Gln Thr Gln Pro Glu Ala Arg Pro Glu
 785 790 795 800
 Ala Glu Leu Pro Lys Lys Gln Glu Lys Ala Gly Trp Phe Arg Phe Pro
 805 810 815
 Lys Leu Gly Phe Ser Ser Ser Pro Thr Lys Lys Ser Lys Ser Thr Glu
 820 825 830
 Asp Gly Ala Glu Leu Glu Glu Gln Lys Leu Gln Glu Glu Thr Ile Thr
 835 840 845
 Phe Phe Asp Ala Arg Glu Ser Phe Ser Pro Glu Glu Lys Glu Glu Gly
 850 855 860
 Glu Leu Ile Gly Pro Val Gly Thr Gly Leu Asp Ser Arg Val Met Val
 865 870 875 880

Thr Ser Ala Ala Arg Thr Glu Leu Ile Leu Pro Glu Gln Asp Arg Lys
885 890 895

Ala Asp Asp Glu Ser Lys Gly Ser Gly Leu Gly Pro Asn Glu Gly
900 905 910

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGTCTCG CCGGGCTGTT CGCGGGCAGG CCCTGCCCTG AAGGGACGAA TCGGCTTGGA	60
GCGCGGGAGG TGGAGTCGGC CCCGGCGGTC GCTCCCTGGA CCCAACCCGA GGCTGACCCA	120
KGCCCTGCC CATGCGGGC GCCCTGGCT CGGAAGAGTC CCCCGGGCCG GGAGCAGCTC	180
CAGGCAGCGG CCCCAGGAGGA AGAGGAAGAA GGGACAGTGC TCAGCTTGGG GGACCCGGAC	240
CCTCGCCGCG GCATTGAG CCGGGGCGAG TCCCGAACTC TGTGCTTGGC ACCGCCGCTC	300
CGAGTAGGGC AGCGCCTGCC GGGACTCTGA CCCGGACCCC CTGCGCCTCG TAGGCGGCGG	360
CGCCGCCGCG CCACCCTGTT CTTCCGTGTC TCCCTCTGCC TGGCGGCAGT CACGGCCAAG	420
AGAGTATTAT GAGGGAGGCC GAGGACTTCA TGCTCCGGAC AGAGAAACGG CGCTGGGATT	480
AGGGATTGCC ACTTCTGAGA GGATGCTGGG AATCTGCAGG GGGAGACGGA AATTCTTGGC	540
TGCCTCGTTG AGTCTTCTCT GCATCCCAGC CATCACCTGG ATTTACCTGT TTTCTGGGAG	600
CTTCGAAGAT GGAAAGCCCG TGTCTCTGTC ACCGCTGGAG TCCCAGGCAC ACAGCCCCAG	660
GTACACGGCC TCCAGCCAGC GGGAGCGCGA GAGCCTGGAG GTGCGCATGC GCGAGGTGGA	720
GGAGGAGAAC CGCGCCCTCC GCAGGCAGCT CAGCCTGGCC CAGGGCCGAG CCCCATCCCA	780
TCGCCGAGGC AACCCTCCA AGACCTACTC CATGGAGGAG GGCCTGGAG ACAGCGAGAA	840
CCTTCGGGCT GGCATCGTGG CAGGCAACAG CTCCGAGTGT GGGCAGCAGC CGGTCGTGGA	900
GAAATGCGAG ACAATCCACG TTGCTATTGT CTGCGCCGGA TACAATGCCA GCCGGGATGT	960
CGTCACCCTG GTCAAATCCG TCCTGTTCCA TAGACGGAAC CCTCTGCACT TCCACCTTAT	1020
TGCTGACTCC ATTGCGGAGC AGATCCTGGC CACGCTCTTC CAGACCTGGA TGGTGCCCGC	1080

TGTGCGTGTG	GACTTCTACA	ATGCAGACGA	GCTCAAGTCT	GAAGTTTCCT	GGATCCCCAA	1140
TAAACATTAC	TCTGGGATTT	ATGGTCTGAT	GAAGCTTGTC	CTGACCAAGA	CTCTTCCTGC	1200
CAACCTGGAG	AGAGTCATCG	TCCTTGACAC	GGATATCACC	TTTGCCACTG	ACATTGCAGA	1260
GCTGTGGGCT	GTGTTCCACA	AGTTCAAAGG	TCAGCAAGTC	CTGGGCTTGG	TGGAGAACCA	1320
GAGTGACTGG	TACCTTGGA	ACCTGTGGAA	AAATCACCGC	CCATGGCCAG	CCCTTGGAAG	1380
AGGCTACAAC	ACAGGGGTGA	TCCTGTTACT	TCTGGATAAG	CTGCGGAAGA	TGAAATGGGA	1440
GCAGATGTGG	AGGCTGACCG	CAGAGAGGGA	GCTCATGGGC	ATGCTCTCTA	CATCCTTAGC	1500
TGACCAGGAT	ATTTTCAATG	CCGTCATCAA	ACAAAACCCC	TTCCTTGTGT	ACCAGCTCCC	1560
CTGCTTCTGG	AATGTGCAGC	TGTCAGACCA	CACCCGCTCC	GAGCAGTGCT	ACAGAGACGT	1620
GTCTGATCTA	AAGGTCATTC	ACTGGAAGTC	CCCCAAGAAG	CTCCGGGTGA	AGAACAAGCA	1680
TGTGGAGTTT	TTTCGCAACC	TCTACCTGAC	CTTCCTGGAG	TATGACGGCA	ATCTTCTGAG	1740
GCGGGAAGTG	TTTGGCTGCC	CCAGTGAGGC	TGATGTCAAC	AGTGAAAACC	TCCAGAAGCA	1800
GCTGTCTGAG	CTGGACGAGG	ACGACCTGTG	CTATGAGTTC	CGGCGAGAGC	GCTTCACTGT	1860
CCACCGCACC	CACCTGTACT	TCCTGCACTA	CGAGTATGAG	CCTGCAGCAG	ACAGCACGGA	1920
CGTCACCCTG	GTCGCTCAGC	TGTCCATGGA	CAGGCTCCAG	ATGCTGGAGG	CCATCTGCAA	1980
GCACTGGGAG	GGGCCCATCA	GCCTGGCCCT	CTACCTGTCA	GACGCCGAGG	CCCAGCAGTT	2040
CCTCCGCTAC	GCACAGGGCT	CTGAGGTGCT	TATGAGCCGC	CACAACGTGG	GCTACCACAT	2100
CGTGTAACAAG	GAGGGCCAGT	TCTACCCCGT	GAACCTGCTG	CGCAACGTGG	CCATGAAGCA	2160
CATCAGCACT	CCCTACATGT	TCCTGTCTGA	CATTGACTTC	CTGCCCATGT	ATGGGCTCTA	2220
TGAGTACCTC	AGGAAGTCTG	TCATCCAGCT	CGATCTTGCC	AACACCAAGA	AAGCAATGAT	2280
TGTCCCCGCG	TTGAGACAC	TGCGCTACCG	GCTGTCCCTTC	CCCAAGTCAA	AAGCGGAGTT	2340
GCTGTCAATG	CTGGACATGG	GGACCCTCTT	CACATTCAGG	TACCACGTCT	GGACGAAAGG	2400
CCACGCACCC	ACAAACTTCG	CCAAGTGGCG	GACCGCCACC	ACGCCTTACC	GGGTTGAGTG	2460
GGAGGCCGAT	TTTGAGCCGT	ATGTTGTTGT	GAGACGTGAC	TGCCCCGAGT	ACGACCGGAG	2520
GTTTGTAGGC	TTTGGCTGGA	ACAAAGTGGC	TCATATCATG	GAGCTGGATG	TGCAGGAGTA	2580
TGAGTTCATT	GTGCTGCCCCA	ACGCCTACAT	GATCCACATG	CCTCATGCCC	CCAGCTTCGA	2640
CATTACCAAG	TTCCGTTCCA	ACAAGCAATA	CCGCATCTGT	CTCAAAACCC	TCAAGGAAGA	2700
GTTTCAGCAG	GACATGTCCC	GCCGCTACGG	CTTTGCTGCC	CTGAAATATC	TCACAGCCGA	2760
GAACAACAGC	TAGCACCAAG	AAGCCCACCA	CTAGGGGGAG	ACATGCTGTA	GGGGAAGTGC	2820

CACTCGCTGT TTGGGGCCCCG GCCTTCAAAT TCAAAATTGA GCCATGCTTT TTCGGTTTGT	2880
TTTTATTAT CTCTTTGGCC CAGCCAAGCT GCCCTCACTA CAGAGACCTT GGACAAGGAT	2940
CCAGCCAGTC CCTCTCTGCC CCACAACCCT GCATTCCCAG AGGTTAGCTA TGCAGCCCAC	3000
CTAGATGAGT CTCTTCAAGA ATGGGAAATC AAGGGGTGAC AGGGAGTAAA AGGGTTATCA	3060
TCTTACTGCA AAGCCACAAG ATCAGGGCAG GGCTTTAGGA TGTCTGGAT GCTTTTTAAT	3120
AATTATGCTT CCCATCATAA CTGGGGAGAA AGGGAAGTCA GGGTTCTAGG GGTATTTCGT	3180
CCCAGGAAAT AGAAGTGAAA TTGTCTTTAT TAAGTGAAAA CTTTCCCCTT TGCCCTGCAA	3240
TGTAGCTGGG CATTCAAACG GAGGGCAAAC CGATGATCTA AACCAACCAC TTGGAAAAAC	3300
CCAATGGGGA CATTGTAACC AGAGGGTCCT GGAGGTGGGG TTGATGGGTT TCCTTATCCC	3360
CAAAGTCACT CCTGTTTTGT TTTGTTTTTC TTTGGGGGTT TTGTTTATTT TTGGGGCTGG	3420
CAATCCAAAA TAGAAAATCT GATCCTTTGA GGCTCTAAAG GAAAATCAGC TGCCCTTACC	3480
AACCACCCTC TATCAGCAGT GGCCCAGGAA GGAGGTCAAG CATCTTCGGC CGATATTTAA	3540
ACATGGGCAG CTCCTTCAG GATGATCACC GAGGCTCCCG TGACTTTGAA CTCCCTACTC	3600
TCCAGAATCC AGGGGCTATA GCGATGGGGA CTGCGGAATT ACGAGGGCTG GCTGTTTTAC	3660
ACCGGTCACA TTTTCTATTG GCAGTGA CTGATTGGA AAGGGCTTTG AAGGAACTAC	3720
TTCACTGCAC ACACAAGGTA CGAACCTYTC AGGCCTTTTC AAGAACTTTC ATAATTCATG	3780
AAAGCCCAGT TYTGAAGATT CACGTATCCA TYTGAGAGACC TACAGGAAGA AAGTGATTGG	3840
GTCCTCTGG TTCTTGCTG CTCCTACTGT GATGGGAAGA GGTGACAACC TCAGTCTCCC	3900
TTTGGGACCT GTCCAAGGGT AGGCAACCAC CTTACCTTC ACACAGATTG AGGAGACACT	3960
GGACTTTTTA CCCATTTTCT TTAATYTTCA ATATTAATAT TGTGTTTACA TTGATGAGAA	4020
CAAGAGTTAA TGCCCTACCC TCTGCTGGGC TGTTTGTATT GAGTTGCAAT GTGACCAGCG	4080
AAAGCTGCAT TTAATAAATG AAAGTACAGA CTGAAAAAAAA AAAAAAAAAA AAAAAAAAAA	4140
AA	4142

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Leu Gly Ile Cys Arg Gly Arg Arg Lys Phe Leu Ala Ala Ser Leu
1 5 10 15

Ser Leu Leu Cys Ile Pro Ala Ile Thr Trp Ile Tyr Leu Phe Ser Gly
20 25 30

Ser Phe Glu Asp Gly Lys Pro Val Ser Leu Ser Pro Leu Glu Ser Gln
35 40 45

Ala His Ser Pro Arg Tyr Thr Ala Ser Ser Gln Arg Glu Arg Glu Ser
50 55 60

Leu Glu Val Arg Met Arg Glu Val Glu Glu Glu Asn Arg Ala Leu Arg
65 70 75 80

Arg Gln Leu Ser Leu Ala Gln Gly Arg Ala Pro Ser His Arg Arg Gly
85 90 95

Asn His Ser Lys Thr Tyr Ser Met Glu Glu Gly Thr Gly Asp Ser Glu
100 105 110

Asn Leu Arg Ala Gly Ile Val Ala Gly Asn Ser Ser Glu Cys Gly Gln
115 120 125

Gln Pro Val Val Glu Lys Cys Glu Thr Ile His Val Ala Ile Val Cys
130 135 140

Ala Gly Tyr Asn Ala Ser Arg Asp Val Val Thr Leu Val Lys Ser Val
145 150 155 160

Leu Phe His Arg Arg Asn Pro Leu His Phe His Leu Ile Ala Asp Ser
165 170 175

Ile Ala Glu Gln Ile Leu Ala Thr Leu Phe Gln Thr Trp Met Val Pro
180 185 190

Ala Val Arg Val Asp Phe Tyr Asn Ala Asp Glu Leu Lys Ser Glu Val
195 200 205

Ser Trp Ile Pro Asn Lys His Tyr Ser Gly Ile Tyr Gly Leu Met Lys
210 215 220

Leu Val Leu Thr Lys Thr Leu Pro Ala Asn Leu Glu Arg Val Ile Val
225 230 235 240

Leu Asp Thr Asp Ile Thr Phe Ala Thr Asp Ile Ala Glu Leu Trp Ala
245 250 255

Val Phe His Lys Phe Lys Gly Gln Gln Val Leu Gly Leu Val Glu Asn
260 265 270

Gln Ser Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp

275					280					285				
Pro	Ala	Leu	Gly	Arg	Gly	Tyr	Asn	Thr	Gly	Val	Ile	Leu	Leu	Leu
290					295					300				
Asp	Lys	Leu	Arg	Lys	Met	Lys	Trp	Glu	Gln	Met	Trp	Arg	Leu	Thr
305					310					315				320
Glu	Arg	Glu	Leu	Met	Gly	Met	Leu	Ser	Thr	Ser	Leu	Ala	Asp	Gln
				325					330					335
Ile	Phe	Asn	Ala	Val	Ile	Lys	Gln	Asn	Pro	Phe	Leu	Val	Tyr	Gln
			340					345					350	
Pro	Cys	Phe	Trp	Asn	Val	Gln	Leu	Ser	Asp	His	Thr	Arg	Ser	Glu
			355				360					365		
Cys	Tyr	Arg	Asp	Val	Ser	Asp	Leu	Lys	Val	Ile	His	Trp	Asn	Ser
370							375					380		Pro
Lys	Lys	Leu	Arg	Val	Lys	Asn	Lys	His	Val	Glu	Phe	Phe	Arg	Asn
385							390					395		400
Tyr	Leu	Thr	Phe	Leu	Glu	Tyr	Asp	Gly	Asn	Leu	Leu	Arg	Arg	Glu
				405					410					415
Phe	Gly	Cys	Pro	Ser	Glu	Ala	Asp	Val	Asn	Ser	Glu	Asn	Leu	Gln
			420					425					430	Lys
Gln	Leu	Ser	Glu	Leu	Asp	Glu	Asp	Asp	Leu	Cys	Tyr	Glu	Phe	Arg
			435				440					445		Arg
Glu	Arg	Phe	Thr	Val	His	Arg	Thr	His	Leu	Tyr	Phe	Leu	His	Tyr
			450				455					460		Glu
Tyr	Glu	Pro	Ala	Ala	Asp	Ser	Thr	Asp	Val	Thr	Leu	Val	Ala	Gln
465							470					475		480
Ser	Met	Asp	Arg	Leu	Gln	Met	Leu	Glu	Ala	Ile	Cys	Lys	His	Trp
				485					490					495
Gly	Pro	Ile	Ser	Leu	Ala	Leu	Tyr	Leu	Ser	Asp	Ala	Glu	Ala	Gln
			500					505					510	
Phe	Leu	Arg	Tyr	Ala	Gln	Gly	Ser	Glu	Val	Leu	Met	Ser	Arg	His
			515				520					525		Asn
Val	Gly	Tyr	His	Ile	Val	Tyr	Lys	Glu	Gly	Gln	Phe	Tyr	Pro	Val
			530				535					540		Asn
Leu	Leu	Arg	Asn	Val	Ala	Met	Lys	His	Ile	Ser	Thr	Pro	Tyr	Met
545							550					555		560
Leu	Ser	Asp	Ile	Asp	Phe	Leu	Pro	Met	Tyr	Gly	Leu	Tyr	Glu	Tyr
				565					570				575	Leu
Arg	Lys	Ser	Val	Ile	Gln	Leu	Asp	Leu	Ala	Asn	Thr	Lys	Lys	Ala
														Met

580	585	590
Ile Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Leu Ser Phe Pro Lys 595	600	605
Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr 610	615	620
Phe Arg Tyr His Val Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala 625	630	635
Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp 645	650	655
Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg 660	665	670
Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu 675	680	685
Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile 690	695	700
His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn 705	710	715
Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln 725	730	735
Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala 740	745	750
Glu Asn Asn Ser 755		

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGCACCGGTG GTCGGCTGTT GGGTGTGGAG TTTCCCAGCG CCCCTCGGGT CCGACCCCTTT	60
GAGCGTTCTG CTCCGGCGCC AGCCTACCTC GTCCTCGGC GCCATGACCA CAACCACCAC	120
CTTCAAGGGA GTCGACCCCA ACAGCAGGAA TAGCTCCCGA GTTTTGCGGC CTCCAGGTGG	180
TGGATCCAAT TTTTCATTAG GTTTTGATGA ACCAACAGAA CAACCTGTGA GGAAGAACAA	240

AATGGCCTCT AATATCTTTG GGACACCTGA AGAAAATCAA GCTTCTTGGG CCAAGTCAGC	300
AGGTGCCAAG TCTAGTGGTG GCAGGGAAGA CTTGGAGTCA TCTGGACTGC AGAGAAGGAA	360
CTCCTCTGAA GCAAGCTCCG GAGACTTCTT AGATCTGAAG GGAGAAGGTG ATATTCATGA	420
AAATGTGGAC ACAGACTTGC CAGGCAGCCT GGGGCAGAGT GAAGAGAAGC CCGTGCCTGC	480
TGCGCCTGTG CCCAGCCCGG TGGCCCCGGC CCCAGTGCCA TCCAGAAGAA ATCCCCCTGG	540
CGGCAAGTCC AGCCTCGTCT TGGGTTAGCT CTGACTGTCC TGAACGCTGT CGTTCTGTCT	600
GTTTCCTCCA TGCTTGTGAA CTGCACAACT TGAGCCTGAC TGTACATCTC TTGGATTGTG	660
TTCATTAAAA AGAAGCACTT TATGTACTGC TGTCTTTTTT TTTTTTCTT TTGAAGAACA	720
GGTTTCTCTC TGTCTTGAC TCTTGGGTCT GTGGGCCATG GCATGAGTGT TTTCTAGTAG	780
TAGATTGGAG GGAAAGCTTT GTGACACTTA GTACTGTGTT TTTAAGAAGA AATAATTGG	840
TTCCAGATGT GTTAGAGGAT CTTTTGTACT GAGGTTTTTA ACACCTTACT TGGGTTTACC	900
AAGCCTCAAC TGGACAGACC ATAAACAGTC CACAGGCACC GTTCCTGCCA GGCCCCAACC	960
CACAGGGAGT CTCTCCGAG AGCCTTCTTG GTGTTGCCCT AACTTGCCAG TGGCCTTTGC	1020
TCAGAGCCTC CTCCTGTGAC ATGTGAACAA TGAAGAGGCC TGCGCYTCCT GCCTTGCCGC	1080
CTGCAAAGCA AAGAACTGC CTTTATTTT TTAACCTTAA AAAGTAGCCA GATAGTAACA	1140
AGACTGGCTG GCTGATGAGC AAAGCYTTTG CTCTCACGCA GAGGAAGGCT TGGATGTACA	1200
ATGAAACTGC CTGGAATAA AAGCAGTGAA GCAAGGGAGG CAATCACACT GAAGCGGGTC	1260
TTCTCCAGG AACGGGTCC CACAGGCGTG TTGTTTTAAA TAACCTGATG CTGTGTGCAT	1320
GATGCTGGTG CTTGACCATG AAAGGAAAGT CTCATCCTTA AAATGTGTTG TACTTCACAA	1380
TCCTGGACTG TTGCTTCAAG TAAACAATAT CCACATTTTG AAAAAAAAAA AAAAA	1435

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Thr Thr Thr Thr Thr Phe Lys Gly Val Asp Pro Asn Ser Arg Asn

1	5	10	15
Ser Ser Arg Val Leu Arg Pro Pro Gly Gly Gly Ser Asn Phe Ser Leu			
20	25	30	
Gly Phe Asp Glu Pro Thr Glu Gln Pro Val Arg Lys Asn Lys Met Ala			
35	40	45	
Ser Asn Ile Phe Gly Thr Pro Glu Glu Asn Gln Ala Ser Trp Ala Lys			
50	55	60	
Ser Ala Gly Ala Lys Ser Ser Gly Gly Arg Glu Asp Leu Glu Ser Ser			
65	70	75	80
Gly Leu Gln Arg Arg Asn Ser Ser Glu Ala Ser Ser Gly Asp Phe Leu			
85	90	95	
Asp Leu Lys Gly Glu Gly Asp Ile His Glu Asn Val Asp Thr Asp Leu			
100	105	110	
Pro Gly Ser Leu Gly Gln Ser Glu Glu Lys Pro Val Pro Ala Ala Pro			
115	120	125	
Val Pro Ser Pro Val Ala Pro Ala Pro Val Pro Ser Arg Arg Asn Pro			
130	135	140	
Pro Gly Gly Lys Ser Ser Leu Val Leu Gly			
145	150		

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGCGTCGCG CGCGCTACCA CACCCAGGTT CGGCCCGTAG GCGTCTGGCA GCCCGGCGCC	60
ATCTTCATCG AGCGCCATGG CCGCAGCCTG CGGGCCGGGA GCGGCCGGGT ACTGCTTGCT	120
CCTCGGCTTG CATTTGTTTC TGCTGACCGC GGGCCCTGCC CTGGGCTGGA ACGACCTGA	180
CAGAATGTTG CTGCGGGATG TAAAAGCTCT TACCCTCCAC TATGACCGCT ATACCACCTC	240
CCGCAGGCTG GATCCCATCC CACAGTTGAA ATGTGTTGGA GGCACAGCTG GTTGTGATTC	300
TTATACCCCA AAAGTCATAC AGTGTCAGAA CAAAGGCTGG GATGGGTATG ATGTACAGTG	360
GGAATGTAAG ACGGACTTAG ATATTGCATA CAAATTTGGA AAAACTGTGG TGAGCTGTGA	420

AGGCTATGAG TCCTCTGAAG ACCAGTATGT ACTAAGAGGT TCTTGTGGCT TGGAGTATAA	480
TTTAGATTAT ACAGAACTTG GCCTGCAGAA ACTGAAGGAG TCTGGAAAGC AGCACGGCTT	540
TGCCTCTTTC TCTGATTATT ATTATAAGTG GTCCTCGGCG GATTCCTGTA ACATGAGTGG	600
ATTGATTACC ATCGTGGTAC TCCTTGGGAT CGCCTTTGTA GTCTATAAGC TGTTCTGAG	660
TGACGGGCAG TATTCTCCTC CACCGTACTC TGAGTATCCT CCATTTTCCC ACCGTTACCA	720
GAGATTCACC AACTCAGCAG GACCTCCTCC CCCAGGCTTT AAGTCTGAGT TCACAGGACC	780
ACAGAATACT GGCCATGGTG CAACTTCTGG TTTTGGCAGT GCTTTTACAG GACAACAAGG	840
ATATGAAAAT TCAGGACCAG GGTTCCTGGAC AGGCTTGGGA ACTGGTGGAA TACTAGGATA	900
TTTGTTTGGC AGCAATAGAG CGGCAACACC CTTCTCAGAC TCGTGGTACT ACCCGTCTTA	960
TCCTCCCTCC TACCCTGGCA CGTGGAATAG GGCTTACTCA CCCCTTCATG GAGGCTCGGG	1020
CAGCTATTCG GTATGTTCAA ACTCAGACAC GAAAACCAGA ACTGCATCAG GATATGGTGG	1080
TACCAGGAGA CGATAAAGTA GAAAGTTGGA GTCAAACACT GGATGCAGAA ATTTTGGATT	1140
TTTCATCACT TTCTCTTAG AAAAAAAGTA CTACCTGTTA ACAATTGGGA AAAGGGGATA	1200
TTCAAAAGTT CTGTGGTGTT ATGTCCAGTG TAGCTTTTGT TATTCTATTA TTTGAGGCTA	1260
AAAGTTGATG TGTGACAAA TACTTATGTG TTGTATGTCA GTGTAACATG CAGATGTATA	1320
TTGCAGTTT KGAAAGTGAT CATTACTGTG GAATGCTAAA AATACATTAA TTTCTAAAC	1380
CTGTGATGCC CTAAGAAGCA TTAAGAATGA AGGTGTTGTA CTAATAGAAA CTAAGTACAG	1440
AAAATTCAG TTTTAGGTGG TTGTAGCTGA TGAGTTATTA CCTCATAGAG ACTATAATAT	1500
TCTATTTGGT ATTATATTAT TTGATGTTG CTGTTCTTCA AACATTTAAA TCAAGCTTG	1560
GACTAATTAT GCTAATTGT GAGTTCTGAT CACTTTTGAG CTCTGAAGCT TTGAATCATT	1620
CAGTGGTGA GATGGCCTTC TGGTAACTGA ATATTACCTT CTGTAGGAAA AGGTGGAAAA	1680
TAAGCATCTA GAAGGTTGTT GTGAATGACT CTGTGCTGGC AAAAATGCTT GAAACCTCTA	1740
TATTTCTTTC GTTCATAAGA GGTAAAGGTC AAATTTTCA ACAAAGTCT TTTAATAACA	1800
AAAGCATGCA GTTCTCTGTG AAATCTCAAA TATTGTTGTA ATAGTCTGTT TCAATCTTAA	1860
AAAGAATCAA TAAAAACAAA CAAGGAAAAA AAAAAAAAAA AAAA	1904

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Ala	Ala	Ala	Cys	Gly	Pro	Gly	Ala	Ala	Gly	Tyr	Cys	Leu	Leu	Leu		
1				5					10					15			
Gly	Leu	His	Leu	Phe	Leu	Leu	Thr	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Asn		
			20					25					30				
Asp	Pro	Asp	Arg	Met	Leu	Leu	Arg	Asp	Val	Lys	Ala	Leu	Thr	Leu	His		
		35					40					45					
Tyr	Asp	Arg	Tyr	Thr	Thr	Ser	Arg	Arg	Leu	Asp	Pro	Ile	Pro	Gln	Leu		
	50					55					60						
Lys	Cys	Val	Gly	Gly	Thr	Ala	Gly	Cys	Asp	Ser	Tyr	Thr	Pro	Lys	Val		
65					70					75					80		
Ile	Gln	Cys	Gln	Asn	Lys	Gly	Trp	Asp	Gly	Tyr	Asp	Val	Gln	Trp	Glu		
				85					90					95			
Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	Lys	Phe	Gly	Lys	Thr	Val	Val		
			100					105					110				
Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly		
		115					120					125					
Ser	Cys	Gly	Leu	Glu	Tyr	Asn	Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln		
	130					135					140						
Lys	Leu	Lys	Glu	Ser	Gly	Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp		
145					150					155					160		
Tyr	Tyr	Tyr	Lys	Trp	Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu		
			165						170					175			
Ile	Thr	Ile	Val	Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu		
			180					185						190			
Phe	Leu	Ser	Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro		
		195					200					205					
Pro	Phe	Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro		
	210					215					220						
Pro	Pro	Gly	Phe	Lys	Ser	Glu	Phe	Thr	Gly	Pro	Gln	Asn	Thr	Gly	His		
225					230					235					240		
Gly	Ala	Thr	Ser	Gly	Phe	Gly	Ser	Ala	Phe	Thr	Gly	Gln	Gln	Gly	Tyr		
			245						250					255			
Glu	Asn	Ser	Gly	Pro	Gly	Phe	Trp	Thr	Gly	Leu	Gly	Thr	Gly	Gly	Ile		

260	265	270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp		
275	280	285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn		
290	295	300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys		
305	310	315
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr		
325	330	335
Arg Arg Arg		

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTGTCTGGCG GCGGCAGCAT GCGGCGGGG GCGGCTGAGG CAGCTGTAGC GGCCGTGGAG	50
GAGGTCGGCT CAGCCGGGCA GTTTGAGGAG CTGCTGCGCC TCAAAGCCAA GTCCCTCCTT	120
GTGGTCCATT TCTGGGCACC ATGGGCTCCA CAGTGTGCAC AGATGAACGA AGTTATGGCA	180
GAGTTAGCTA AAGAACTCCC TCAAGTTTCA TTTGTGAAGT TGGAAGCTGA AGGTGTTCTT	240
GAAGTATCTG AAAAATATGA AATTAGCTCT GTTCCCACTT TTCTGTTTTT CAAGAATTCT	300
CAGAAAATCG ACCGATTAGA TGGTGCACAT GCCCCAGAGT TGACCAAAAA AGTTCAGCGA	360
CATGCATCTA GTGGCTCCTT CCTACCCAGC GCTAATGAAC ATCTTAAAGA AGACCTCAGC	420
CTTCGCCTGA AAAAGCTGAC TCACGCTGCC CCCTGCATGC TGTTTCATGAA GGAACACCT	480
CAAGAACCAC GCTGTGGTTT CAGCAAGCAG ATGGTGGAAT TCCTTCACAA ACACAATATT	540
CAGTTCAGCA GCTTTGATAT CTTCTCAGAT GAAGAAGTTC GACAGGGGCT CAAAACGTAC	600
TCTAATTGGC CCACCTATCC TCAGCTCTAT GTTTCTGGAG AGCTAATAGG AGGACTTGAC	660
ATAATTAAGG AGCTGGAAGC ATCAGAAGAG CTGGACACGA TCTGTCCCAA AGCTCCCAA	720
TTAGAGGAAA GGCTCAAAGT GCTGACAAAT AAAGCTTCTG TGATGCTCTT TATGAAAGGA	780

AACAAACAGG AAGCAAAATG TGGATTCAGC AAACAAATTC TGGAAATACT AAATAGTACT	840
GGTGTGTAAT ATGAAACATT CGATATATTG GAGGATGAAG AAGTTCGGCA AGGATTAAAA	900
GCTTACTCAA ATTGGCCAAC ATACCCTCAG CTGTATGTGA AAGGGGAGCT GGTGGGAGGA	960
TTGGATATTG TGAAGGAACT GAAAGAAAAT GGTGAATTGC TGCCTATACT GAGAGGAGAA	1020
AATTAATAAA TCTTAAACTT GGTGCCCAAC TATTGTAAGA AATATTTAAT TACATTGGGA	1080
GCAGTTCATG ATTTAGTCCT CAGAAATGGA CTAGGAATAG AAAATTCCTG CTTTCTCAGT	1140
TACATGTTTT GTGTATTTC CAATGTCGTG CTAAATAAAT GTATGTTACA TTTTTTCCC	1200
ACCAAAAATA GAATGCAATA AACATCTTCA AATTATTAAC AATAAAAAAA AAAAAAAAAA	1260

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Ala	Ala	Gly	Ala	Ala	Glu	Ala	Ala	Val	Ala	Ala	Val	Glu	Glu	Val	1	5	10	15
Gly	Ser	Ala	Gly	Gln	Phe	Glu	Glu	Leu	Leu	Arg	Leu	Lys	Ala	Lys	Ser	20	25	30	
Leu	Leu	Val	Val	His	Phe	Trp	Ala	Pro	Trp	Ala	Pro	Gln	Cys	Ala	Gln	35	40	45	
Met	Asn	Glu	Val	Met	Ala	Glu	Leu	Ala	Lys	Glu	Leu	Pro	Gln	Val	Ser	50	55	60	
Phe	Val	Lys	Leu	Glu	Ala	Glu	Gly	Val	Pro	Glu	Val	Ser	Glu	Lys	Tyr	65	70	75	80
Glu	Ile	Ser	Ser	Val	Pro	Thr	Phe	Leu	Phe	Phe	Lys	Asn	Ser	Gln	Lys	85	90	95	
Ile	Asp	Arg	Leu	Asp	Gly	Ala	His	Ala	Pro	Glu	Leu	Thr	Lys	Lys	Val	100	105	110	
Gln	Arg	His	Ala	Ser	Ser	Gly	Ser	Phe	Leu	Pro	Ser	Ala	Asn	Glu	His	115	120	125	

Leu	Lys	Glu	Asp	Leu	Ser	Leu	Arg	Leu	Lys	Lys	Leu	Thr	His	Ala	Ala	
130						135					140					
Pro	Cys	Met	Leu	Phe	Met	Lys	Gly	Thr	Pro	Gln	Glu	Pro	Arg	Cys	Gly	
145					150					155					160	
Phe	Ser	Lys	Gln	Met	Val	Glu	Ile	Leu	His	Lys	His	Asn	Ile	Gln	Phe	
				165					170					175		
Ser	Ser	Phe	Asp	Ile	Phe	Ser	Asp	Glu	Glu	Val	Arg	Gln	Gly	Leu	Lys	
			180					185					190			
Thr	Tyr	Ser	Asn	Trp	Pro	Thr	Tyr	Pro	Gln	Leu	Tyr	Val	Ser	Gly	Glu	
	195						200					205				
Leu	Ile	Gly	Gly	Leu	Asp	Ile	Ile	Lys	Glu	Leu	Glu	Ala	Ser	Glu	Glu	
210					215					220						
Leu	Asp	Thr	Ile	Cys	Pro	Lys	Ala	Pro	Lys	Leu	Glu	Glu	Arg	Leu	Lys	
225					230					235					240	
Val	Leu	Thr	Asn	Lys	Ala	Ser	Val	Met	Leu	Phe	Met	Lys	Gly	Asn	Lys	
				245					250					255		
Gln	Glu	Ala	Lys	Cys	Gly	Phe	Ser	Lys	Gln	Ile	Leu	Glu	Ile	Leu	Asn	
			260					265					270			
Ser	Thr	Gly	Val	Glu	Tyr	Glu	Thr	Phe	Asp	Ile	Leu	Glu	Asp	Glu	Glu	
		275					280					285				
Val	Arg	Gln	Gly	Leu	Lys	Ala	Tyr	Ser	Asn	Trp	Pro	Thr	Tyr	Pro	Gln	
	290					295					300					
Leu	Tyr	Val	Lys	Gly	Glu	Leu	Val	Gly	Gly	Leu	Asp	Ile	Val	Lys	Glu	
305					310					315					320	
Leu	Lys	Glu	Asn	Gly	Glu	Leu	Leu	Pro	Ile	Leu	Arg	Gly	Glu	Asn		
				325					330				335			

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTTTTGTGCG ATGCCTACTG GAGACTTTGA TTCGAAGCCC AGTTGGGCCG ACCAGGTGGA	60
GGAGGAGGGG GAGGACGACA AATGTGTCAC CAGCGAGCTC CTCAAGGGGA TCCCTCTGGC	120

CACAGGTGAC ACCAGCCCAG AGCCAGAGCT ACTGCCGGGA GCTCCACTGC CGCCTCCCAA 180
GGAGGTCATC AACGGAAACA TAAAGACAGT GACAGAGTAC AAGATAGATG AGGATGGCAA 240
GAAGTTCAAG ATTGTCCGCA CCTTCAGGAT TGAGACCCGG AAGGCTTCAA AGGCTGTGCG 300
AAGGAGGAAG AACTGGAAGA AGTTCGGGAA CTCAGAGTTT GACCCCCCG GACCCAATGT 360
GGCCACCACC ACTGTCAGTG ACGATGTCTC TATGACGTTT ATCACCAGCA AAGAGGACCT 420
GAACTGCCAG GAGGAGGAGG ACCCTATGAA CAAACTCAAG GGCCAGAAGA TCGTGTCTTG 480
CCGCATCTGC AAGGGCGACC ACTGGACCAC CCGCTGCCCC TACAAGGATA CGCTGGGGCC 540
CATGCAGAAG GAGCTGGCCG AGCAGCTGGG CCTGTCTACT GGCAGAGAAGG AGAAGCTGCC 600
GGGAGAGCTA GAGCCGGTGC AGGCCACGCA GAACAAGACA GGGAAGTATG TGCCGCCGAG 660
CCTGCGCGAC GGGGCCAGCC GCCGCGGGGA GTCCATGCAG CCCACCCGCA GAGCCGACGA 720
CAACGCCACC ATCCGTGTCA CCAACTTGTC AGAGGACACG CGTGAGACCG ACCTGCAGGA 780
GCTCTTCCGG CCTTTCGGCT CCATCTCCCG CATCTACCTG GCTAAGGACA AGACCACTGG 840
CCAATCCAAG GGCTTCGCCT TCATCAGCTT CCACCGCCGC GAGGATGCTG CGCGTGCCAT 900
TGCCGGGGTG TCCGGCTTTG GCTACGACCA CCTCATCTC AACGTCGAGT GGGCCAAGCC 960
GTCCACCAAC TAAGCCAGCT GCCACCGTGT ACTCGGTCCG GGACCCTTGG CGACAGAAGA 1020
CAGCCTCCGA GAGCGCGGGC TCCAAGGGCA ATAAAGCAGC TCCACTCTCA AAAAAAAAAA 1080
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
AAAAAAAAA AA 1152

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
1 5 10 15
Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
20 25 30

Gly	Ile	Pro	Leu	Ala	Thr	Gly	Asp	Thr	Ser	Pro	Glu	Pro	Glu	Leu	Leu	35	40	45	
Pro	Gly	Ala	Pro	Leu	Pro	Pro	Pro	Lys	Glu	Val	Ile	Asn	Gly	Asn	Ile	50	55	60	
Lys	Thr	Val	Thr	Glu	Tyr	Lys	Ile	Asp	Glu	Asp	Gly	Lys	Lys	Phe	Lys	65	70	75	80
Ile	Val	Arg	Thr	Phe	Arg	Ile	Glu	Thr	Arg	Lys	Ala	Ser	Lys	Ala	Val	85	90	95	
Ala	Arg	Arg	Lys	Asn	Trp	Lys	Lys	Phe	Gly	Asn	Ser	Glu	Phe	Asp	Pro	100	105	110	
Pro	Gly	Pro	Asn	Val	Ala	Thr	Thr	Thr	Val	Ser	Asp	Asp	Val	Ser	Met	115	120	125	
Thr	Phe	Ile	Thr	Ser	Lys	Glu	Asp	Leu	Asn	Cys	Gln	Glu	Glu	Glu	Asp	130	135	140	
Pro	Met	Asn	Lys	Leu	Lys	Gly	Gln	Lys	Ile	Val	Ser	Cys	Arg	Ile	Cys	145	150	155	160
Lys	Gly	Asp	His	Trp	Thr	Thr	Arg	Cys	Pro	Tyr	Lys	Asp	Thr	Leu	Gly	165	170	175	
Pro	Met	Gln	Lys	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Leu	Ser	Thr	Gly	Glu	180	185	190	
Lys	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Glu	Pro	Val	Gln	Ala	Thr	Gln	Asn	195	200	205	
Lys	Thr	Gly	Lys	Tyr	Val	Pro	Pro	Ser	Leu	Arg	Asp	Gly	Ala	Ser	Arg	210	215	220	
Arg	Gly	Glu	Ser	Met	Gln	Pro	Thr	Arg	Arg	Ala	Asp	Asp	Asn	Ala	Thr	225	230	235	240
Ile	Arg	Val	Thr	Asn	Leu	Ser	Glu	Asp	Thr	Arg	Glu	Thr	Asp	Leu	Gln	245	250	255	
Glu	Leu	Phe	Arg	Pro	Phe	Gly	Ser	Ile	Ser	Arg	Ile	Tyr	Leu	Ala	Lys	260	265	270	
Asp	Lys	Thr	Thr	Gly	Gln	Ser	Lys	Gly	Phe	Ala	Phe	Ile	Ser	Phe	His	275	280	285	
Arg	Arg	Glu	Asp	Ala	Ala	Arg	Ala	Ile	Ala	Gly	Val	Ser	Gly	Phe	Gly	290	295	300	
Tyr	Asp	His	Leu	Ile	Leu	Asn	Val	Glu	Trp	Ala	Lys	Pro	Ser	Thr	Asn	305	310	315	320

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGAGACCTG GGCTGCTGTG AAAGCCCCTG CACAATCAGC CAGGGAGAAC TGGGCGGGTT	60
TAGTGGCCCC AGGCCCCTC CTCATGCAGC AGTGTGCTGG GGCACAGCT CGTCTCCCCT	120
CTCTTAAGCA CCCGCTTCCT CACCACCCCC ACTGTTGGGC CTATAGTAGC AGGTTAGTGA	180
GTACCTAGGG CGGCTCAACT CCTCCACAG CACCAACCCA GCATGGTCCC ACTGAAGTCC	240
TACTACGCCC TCCCCTCCCC AGCCTTTTCC AGAAACCATA CTGGGCTCAG ATCAGAGCTC	300
CGAAGCGGTC AAAGTGAGCT GAGCAGGACA GGCCAGCCT TTCTCCACTG CCACGTCCCT	360
CATGCACATC ACTCATCTCC TGCTGCAGGC CAAGGCCAAA ATTGGGCTAG TCCTGGCCAG	420
GGAAATCAGA AGCTCTTCTT GGGTGAGATT GAGCCTCCTG TTGCTCCCTG GAGTTCCGGA	480
GGCTGGGCTG CAGCCCCTC AGCTTGCGGG CAAAATACGT GCTCTCCTCT CTCCTTGTC	540
GCTGAGCAAA CCCAGGGAAT AGCCCTCCTC TCCCAGGAA ACTTCTCTGA AATCTTAGAC	600
TTAGCCAGTC TTAGGCCTAC GATGCCACAC AAAGGTTGTT CAGGGAGAAG GGGGTGCAGG	660
AGGCAGAGGG TGCCCCGCAG GGAGCTGGTG GCTCCAGCCC CACTAGAGCT CCTAAAGATC	720
ACACAGCAGC TGCTCCTGAC AGGGATGCTC ATGCCAGAA AGCAAGCCCA GGAGAGGAAG	780
GCAGAGTGTG ACAGAGCAGA GCCAGGGCCA GGCGCACCAG GAGAGGCGTT TCTGGGGCTC	840
CAGGGAAGTG CCACGGGAGG CAGAAGTCCA GAACTGCCCA TATAGATGCC CTTCTACATC	900
CTGGAGCCCA AATCAGTCAT GTGGGTGGGA AGTTCCCAGG GCAGTGGTCA CATCGTGAGA	960
ATTAGCAGGA AAGGCGGGGC CTTTCTTGTC ATAGCTATTT CTGAGGATGA AATGGGAGAC	1020
ATATGCCCAG CACCTGATGT AAGTTTATAT AATGTACCTA CCACTAAGAA ATACATGAAC	1080
CGTGCCATGA GGACAGTAAG TGTTCAATAA GCAACATGAA GCAAGAAACA GTGCAGGGTG	1140
CCCAGTGCAC AACTAGAGA GAAATTGTGA ACATTAAGGA CAAGGAGAAT TGGTGTCTTT	1200
CTAAACATA CTTATTTAAA AACACATACC CACTTACTAA TGTGGAATTA CACAGTTTGT	1260
AACAAGAAAA CAGTCTCTCC CATTCTCTAG TACTGYTCCC CTACCCAGCA GTCAMTTCCA	1320
GTTCAATCAG STATTTTAA AATGTGCTTA TATGACTCTT GCTTGATATA TCAATYTTAG	1380

ACATTACCTG TTGACTCCCT GTTGTCTATC ATGAGGCTTT AGCTCTYTTT TGTCAGCAAC 1440
 CCTCCCCCAT CCCTAGTTAT TAGGTTAAAA AATACTCAGA TTACTATTTC TATTACTATG 1500
 TGAAAGTTAA CTGCGGAGCC AAGAGTTGGA CTATAATTAA ATTACCTTCC TTGTAAAAAA 1560
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1594

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met	Val	Pro	Leu	Lys	Ser	Tyr	Tyr	Ala	Leu	Pro	Ser	Pro	Ala	Phe	Ser	1	5	10	15
Arg	Asn	His	Thr	Gly	Leu	Arg	Ser	Glu	Leu	Arg	Ser	Gly	Gln	Ser	Glu	20	25	30	
Leu	Ser	Arg	Thr	Gly	Pro	Ala	Phe	Leu	His	Cys	His	Val	Pro	His	Ala	35	40	45	
His	His	Ser	Ser	Pro	Ala	Ala	Gly	Gln	Gly	Gln	Asn	Trp	Ala	Ser	Pro	50	55	60	
Gly	Gln	Gly	Asn	Gln	Lys	Leu	Phe	Leu	Gly	Glu	Ile	Glu	Pro	Pro	Val	65	70	75	80
Ala	Pro	Trp	Ser	Ser	Gly	Gly	Trp	Ala	Ala	Ala	His	Ser	Ala	Cys	Gly	85	90	95	
Gln	Asn	Thr	Cys	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Glu	Gln	Thr	Gln	Gly	100	105	110	
Ile	Ala	Leu	Leu	Ser	Pro	Gly	Asn	Phe	Ser	Glu	Ile	Leu	Asp	Leu	Ala	115	120	125	
Ser	Leu	Arg	Pro	Thr	Met	Pro	His	Lys	Gly	Cys	Ser	Gly	Arg	Arg	Gly	130	135	140	
Cys	Arg	Arg	Gln	Arg	Val	Pro	Arg	Arg	Glu	Leu	Val	Ala	Pro	Ala	Pro	145	150	155	160
Leu	Glu	Leu	Leu	Lys	Ile	Thr	Gln	Gln	Leu	Leu	Leu	Thr	Gly	Met	Leu	165	170	175	
Met	Pro	Arg	Lys	Gln	Ala	Gln	Glu	Arg	Lys	Ala	Glu	Cys	Asp	Arg	Ala	180	185	190	

Glu	Pro	Gly	Pro	Gly	Ala	Pro	Gly	Glu	Ala	Phe	Leu	Gly	Leu	Gln	Gly
		195					200					205			
Ser	Ala	Thr	Gly	Gly	Arg	Ser	Pro	Glu	Leu	Pro	Ile				
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TNAATAAACTG GACGGATGCA CTGATAGG

29

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CNCTGATAACA AAGCATTGCC ACTGGCGC

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATCCAGAAA ATTACCGCCG TCCGACCG

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNCTTAGAAGC CTCATTTTG GGAAGTGC

29

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CNGAGAAGACT CAACGAGGCA GCCAAGAA

29

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CNTGCTGACTT GGCCAAGAA GCTTGATT

29

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GNGCTGCTTTC CAGACTCCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ANCCACAGCGT GGTCTTGAG GTGTTCCC

29

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GNTCTTCTGGC CCTTGAGTTT GTTCATAG

29

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GNTGAGCCGCC CTAGGTACTC ACTAACCT

29

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGGCGCCCTC CCTTCCTGAG GAGCTGTTGG CCTGGGTGGG CAGGAACTGC AGTATGGCCA 60
TGGGCTGAGC AGGCTGAGCA CCTCAGCCTT TAGGGCTTAT GGCCAGGGGA CACTGTATGA 120
CTCTCCTCTC CTGCAGGTGT CTATCCACCT GGGGTATGGC ATCTACCGAC CTGTCTCCCT 180
GGGGTCACAT GCTTTGTTTC CATTCTTGTC CTGGCTGGAC CAGCCACTGT GGGACCAACA 240
CCCCCTCCAC ACTCCCCCAG ACTGCTCGTC TATCACCAGG ATCGCTTTGT ACTTTGTGCA 300
AAAGGGTCTG GCTGTCCCTT GCTGTTTTCA TCTTGCCAA GCCTATTGTG CCTCTGGCTG 360
CTGTATGTGT GCGCGTGCAC GTGTGTGTGT TTCATCTGTT CATTCACTGC ACAAGATATT 420
TATTGAGTGC CCACTACGTG CCAGGCACTG TTGCTGAGTT CCTGTGGGTG TGTCTCTCGA 480
TGCCACTCCT GCTTCTCTGG GGGCCTCTTT CTGTGCTTCT CTTTGTCCCC AAATTGCTAC 540
CTCTTTGTCA GTCTGGGTGT CTCAGGTTCT GTGTGTCCTT GTGTGCATTT CTGTCTCTCT 600
CTGTCCCTCGT CTCTCTGCAA GGCCCTCTAT TTCTCTCTTT CTTGGTGTCT GTCCTTTGCC 660
CCCTGTGCCC TCTGGATTCT CTGGGTCTAT GTAGGCCCTT GGTCTGCCCT GGGCTCATCA 720
GCCTTCCTGA CCTCCTCCTG CCCTCCCCCT CACTCCCTCC CTGGCTCTGC CAGTCGGTTC 780
CCACGGAGCC ATTTTGTAGCT CTGATCAGCA TGGGAATGTG CCTCGGCCTC CAAGGGGCTT 840
TGTCTGGTG CCCCCGCCCC TGGTCCCAAC CTGATCCCAC GAGGGAGTTG GGACAGGAGG 900
ATTGATGGTG CTCCCTTCC TGCCAGCGTC AGAGGCCCTG GAGAGGGGCT GTCCATGGCA 960
GCTGGTCTTT ATTCCTCCCT CATGAGCACA GGGTCGGGGG GTCCCCATTC TTGGAAGAGG 1020
TTGAGAAGAC TCCTGGGCTT CAGCCTCTCC CACCCAGCCC TGCCCTCAC CTGCCTGCCC 1080
TCCCCTCCCC CACTCTATAC TAGGGACTGG ATCTCAGCCT CTGATCAGTT TCACAAAGTT 1140
TGTTCCTTAA GGAAATCAAA TCCCATTGTC ACCTAACTCT GAAGATCTAA ATAGCCCTTG 1200
GATCAGTACG GGAACCCCAA ATCCACAGG GCCAGATGTG GAGTCTGTGT CTGCCCCCGT 1260

CTTCTCTCCA TCCTCAAAGC CCCCACTTCT CTCCAGGCTG TTTCTTTTTT TATGACTGTA 1320
AACATAGATA GTGCTTTTATT TTGTTAATAA TAAGATAATG ATGAGTAACT TAACCAGCAC 1380
ATTTCTCCTG TTTACACTCG GGGGATTTTT TTGTTTCTG ATGACATAAT AAAGACAGAT 1440
CATTTTCAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1480

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Ala	Arg	Gly	His	Cys	Met	Thr	Leu	Leu	Ser	Cys	Arg	Cys	Leu	Ser	1	5	10	15
Thr	Trp	Gly	Met	Ala	Ser	Thr	Asp	Leu	Ser	Pro	Trp	Gly	His	Met	Leu	20	25	30	
Cys	Phe	His	Ser	Cys	Pro	Gly	Trp	Thr	Ser	His	Cys	Gly	Thr	Asn	Thr	35	40	45	
Pro	Pro	Thr	Leu	Pro	Gln	Thr	Ala	Arg	Leu	Ser	Pro	Gly	Ser	Leu	Cys	50	55	60	
Thr	Leu	Cys	Lys	Arg	Val	Trp	Leu	Ser	Leu	Ala	Val	Phe	Ile	Ser	Ala	65	70	75	80
Lys	Pro	Ile	Val	Pro	Leu	Ala	Ala	Val	Cys	Val	Arg	Val	His	Val	Cys	85	90	95	
Val	Phe	His	Leu	Phe	Ile	His	Cys	Thr	Arg	Tyr	Leu	Leu	Ser	Ala	His	100	105	110	
Tyr	Val	Pro	Gly	Thr	Val	Ala	Glu	Phe	Leu	Trp	Val	Cys	Leu	Ser	Met	115	120	125	
Pro	Leu	Leu	Leu	Leu	Trp	Gly	Pro	Leu	Ser	Val	Leu	Leu	Phe	Val	Pro	130	135	140	
Lys	Leu	Leu	Pro	Leu	Cys	Gln	Ser	Gly	Cys	Leu	Arg	Phe	Cys	Val	Ser	145	150	155	160
Leu	Cys	Ala	Phe	Leu	Ser	Leu	Ser	Val	Leu	Val	Ser	Leu	Gln	Gly	Pro	165	170	175	
Leu	Phe	Leu	Ser	Phe	Leu	Val	Ser	Val	Leu	Cys	Pro	Leu	Cys	Pro	Leu				

180	185	190
Asp Ser Leu Gly Leu Cys Arg	Pro Leu Val Cys Pro Gly Leu Ile Ser	
195	200	205
Leu Pro Asp Leu Leu Leu Pro Ser Pro Ser Leu Pro Pro Trp Leu Cys		
210	215	220
Gln Ser Val Pro Thr Glu Pro Phe Leu Ala Leu Ile Ser Met Gly Met		
225	230	235
Cys Leu Gly Leu Gln Gly Ala Leu Ser Trp Cys Pro Arg Pro Trp Ser		
245	250	255
Gln Pro Asp Pro Thr Arg Glu Leu Gly Gln Glu Asp		
260	265	

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCCGGCGGCT CCTGGAACCC CGGTTGCGGG CGATGCCAGC CACCCAGCG AAGCCGCCGC	60
AGTTCAGTGC TTGGATAATT TGAAAGTACA ATAGTTGGTT TCCCTGTCCA CCCGCCAC	120
TTCGCTTGCC ATCACAGCAC GCCTATCGGA TGTGAGAGGA GAAGTCCCGC TGCTCGGGCA	180
CTGTCTATAT ACGCCTAACA CCTACATATA TTTTAAAAAC ATTAAATATA ATTAACAATC	240
AAAAGAAAGA GGAGAAAGGA AGGGAAGCAT TACTGGGTGA CTATGCACTT GCGACTGATT	300
TCTTGGCTTT TTATCATTTT GAACTTTATG GAATACATCG GCAGCCAAA CGCCTCCCGG	360
GGAAGGCGCC AGCGAAGAAT GCATCCTAAC GTTAGTCAAG GCTGCCAAGG AGGCTGTGCA	420
ACATGCTCAG ATTACAATGG ATGTTTGTC TGTAAAGCCA GACTATTTT TGCTCTGGAA	480
AGAATTGGCA TGAAGCAGAT TGGAGTATGT CTCTCTTCAT GTCCAAGTGG ATATTATGGA	540
ACTCGATATC CAGATATAAA TAAGTGACAA AAATGCAAAG CTGACTGTGA TACCTGTTTC	600
AACAAAAATT TCTGCACAAA ATGTAAAAGT GGATTTTACT TACACCTTGG AAAGTGCCTT	660
GACAATTGCC CAGAAGGGTT GGAAGCCAAC AACCATACTA TGGAGTGTGT CAGTATTGTG	720
CACTGTGAGG TCAGTGAATG GAATCCTTGG AGTCCATGCA CGAAGAAGGG AAAACATGT	780

GGCTTCAAAA GAGGGACTGA AACACGGGTC CGAGAAATAA TACAGCATCC TTCAGCAAAG 840
GGTAACCTGT GTCCCCAAC AAATGAGACA AGAAAGTGTA CAGTGCAAAG GAAGAAGTGT 900
CAGAAGGGAG AACGAGGAAA AAAAGGAAGG GAGAGGAAAA GAAAAAAACC TAATAAAGGA 960
GAAAGTAAAG AAGCAATACC TGACAGCAAA AGTCTGGAAT CCAGCAAAGA AATCCCAGAG 1020
CAACGAGAAA ACAAACAGCA GCAGAAGAAG CGAAAAGTCC AAGATAAACA GAAATCGGGG 1080
ATTGAAGTCA CCCTAGCTGA AGGCCTCACC AGTGTTCAC AGAGGACACA GCCCACCCCT 1140
TGCAGGAGGA GGTATCTCTG AGTGTGCAGC ACAGAATCGC ATGACCCACC TTAACCTTCC 1200
TGTTGTCATG GAAGGATGCA CGGCTGCTCT GTCCACTGTG ATTCCTAGCC CTCTCAAGAT 1260
CACTGCTTTC TGAAGAATTT GCAATGACTC TGGCTTCTGG CTGCTTATCT CTGGACACCC 1320
GTTCTCCACC AGTTGTACAG TTCATGTAAT CTAATTGGCT TAATTGATTT TCCACTTCTC 1380
TCTTCCTCTT CTAAGATATA AACATTTTAA ATGATTTAAA AAAAAAAAAA AAAAAA 1436

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	His	Leu	Arg	Leu	Ile	Ser	Trp	Leu	Phe	Ile	Ile	Leu	Asn	Phe	Met
1				5					10					15	
Glu	Tyr	Ile	Gly	Ser	Gln	Asn	Ala	Ser	Arg	Gly	Arg	Arg	Gln	Arg	Arg
			20					25					30		
Met	His	Pro	Asn	Val	Ser	Gln	Gly	Cys	Gln	Gly	Gly	Cys	Ala	Thr	Cys
		35					40					45			
Ser	Asp	Tyr	Asn	Gly	Cys	Leu	Ser	Cys	Lys	Pro	Arg	Leu	Phe	Phe	Ala
	50					55					60				
Leu	Glu	Arg	Ile	Gly	Met	Lys	Gln	Ile	Gly	Val	Cys	Leu	Ser	Ser	Cys
65					70				75					80	
Pro	Ser	Gly	Tyr	Tyr	Gly	Thr	Arg	Tyr	Pro	Asp	Ile	Asn	Lys	Cys	Thr
			85					90					95		
Lys	Cys	Lys	Ala	Asp	Cys	Asp	Thr	Cys	Phe	Asn	Lys	Asn	Phe	Cys	Thr
		100					105						110		
Lys	Cys	Lys	Ser	Gly	Phe	Tyr	Leu	His	Leu	Gly	Lys	Cys	Leu	Asp	Asn

115		120		125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser				
130		135		140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr				
145		150		155
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val				
	165		170	175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro				
	180		185	190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys				
	195		200	205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn				
	210		215	220
Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser				
	225		230	235
Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys				
	245		250	255
Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala				
	260		265	270
Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg				
	275		280	285
Arg Arg Tyr Leu				
	290			

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGTTAAGAGC AGATTAGAAC AGAAATCAGG AGAACTTGGG AAGAAGATCA CTGAGTTAAC	60
ATTGAAAAAT CAGACACTAC AAAAGGAAAT TGAAAAAGTT TATTTGGATA ATAAGCTCCT	120
CAAGGAGCAA GCACATAACT TAACAATTGA AATGAAAAAT CATTATGTTC CTTTAAAAGT	180
AAGTGAAGAC ATGAAAAAGT CACATGATGC AATTATTGAT GATCTTAATA GAAAGCTTTT	240

AGATGTAACA	CAAAAATATA	CAGAAAAGAA	GTTGGAAATG	GAGAAATTGC	TACTGGAAAA	300
TGACAGCTTA	AGTAAGGATG	TAAGCCGCCT	AGAAACTGTG	TTGTACCTC	CTGAGAAACA	360
TGAAAAAGAG	ATAATAGCTC	TGAAATCCAA	TATTGTTGAA	CTTAAGAAAC	AGCTGTCTGA	420
ACTTAAGAAA	AAATGTGGTG	AAGACCAGGA	GAAAATACAC	GCTCTCACAT	CTGAAAACAC	480
TAACTTGAAG	AAGATGATGA	GTAATCAGTA	TGTGCCAGTT	AAAACCCATG	AAGAGGTTAA	540
AATGACACTG	AATGACACGT	TAGCCAAAAC	TAACAGAGAA	TTATTAGATG	TGAAGAAAAA	600
ATTTGAAGAT	ATAAATCAGG	AATTTGTAAA	AATAAAAGAT	AAGAATGAAA	TATTAAAAAG	660
AAACCTGGAA	AACACTCAGA	ACCAAATAAA	AGCTGAGTAC	ATCAGCCTGG	CAGAGCACGA	720
GGCAAAGATG	AGCTCGCTAA	GTCAGAGCAT	GAGAAAGGTG	CAGGATAGTA	ATGCTGAAAT	780
CTTGGCCAAC	TACAGAAAAG	GCCAAGAAGA	GATTGTGACA	CTGCATGCCG	AAATTAAAGC	840
CCAGAAGAAG	GAGCTCGACA	CAATACAAGA	ATGCATTAAG	GTAAAAATATG	CCCCAATTGT	900
CAGCTTTGAG	GAGTGCGAGA	GAAAATTTAA	AGCAACAGAG	AAAGAACTAA	AAGACCAGTT	960
ATCAGAGCAG	ACACAAAAGT	ATAGTGTCAG	TGAAGAAGAA	GTCAAGAAAA	ACAAGCAAGA	1020
GAATGACAAG	TTAAGAAGG	AGATTTTTAC	CCTTCAGAAA	GATTTGAGAG	ATAAGACAGT	1080
TCTCATTGAG	AAGTCTCATG	AAATGGAAAG	AGCATTAAAG	AGAAAAACAG	ACGAGCTAAA	1140
CAAACAGTTA	AAAGACTTGT	CACAGAAATA	CACGGAAGTA	AAGAATGTGA	AAGAGAAGCT	1200
AGTAGAAGAA	AATGCCAAAC	AGACTTCTGA	GATACTTGCA	GTGCAAAATC	TTTTGCAAAA	1260
ACAACATGTT	CCATTGGAAC	AGGTTGAGGC	TCTGAAAAAA	TCTCTTAATG	GCACAATTGA	1320
AAATCTAAAG	GAAGAACTGA	AGAGTATGCA	AAGGTGTTAC	GAGAAAGAGC	AGCAGACAGT	1380
GACCAAACCTG	CATCAATTGT	TGGAGAAATCA	AAAGAACTCT	TCTGTACCCC	TGGCAGAGCA	1440
TTTGCAGATT	AAAGAAGCAT	TTGAGAAAGA	AGTTGGAATC	ATAAAAGCCA	GCTTGAGAGA	1500
AAAGGAAGAA	GAAAGCCAAA	ACAAAATGGA	AGAAGTCTCC	AACTTCAGT	CGGAGGTTCA	1560
GAATACTAAA	CAAGCATTA	AAAAATTAGA	GACTAGAGAG	GTAGTTGACT	TGTCTAAATA	1620
TAAAGCAACA	AAAAGTGATT	TGGAGACACA	GATTTCTAGC	TTAAATGAAA	AATTGGCCAA	1680
TCTGAATAGA	AAGTATGAGG	AAGTATGTGA	GGAAGTTTTG	CATGCCAAAA	AGAAGGAAAT	1740
ATCTGCAAAA	GATGAGAAGG	AATTACTGCA	TTTCAGCATT	GAGCAAGAAA	TTAAGGATCA	1800
GAAGGAACGA	TGTGATAAGT	CCTTAACAAC	AATCACAGAG	TTACAAAGAA	GAATACAAGA	1860
ATCTGCTAAA	CAAATAGAAG	CAAAAGATAA	TAAGATAACT	GAACTGCTTA	ATGATGTGGA	1920
AAGATTAAAA	CAGGCACTCA	ATGGCCTTTC	CCAACCTACC	TACACAAGTG	GGAACCCAC	1980

CAAGAGGCAG AGCCAGCTGA TTGACACTCT GCAGCACCAA GTGAAATCTC TGGAGCAACA 2040
GCTGGCCGAT GCTGACAGAC AGCACCAAGA AGTAATTGCA ATTTATCGGA CACACCTTCT 2100
TAGTGCTGCA CAGGGTCACA TGGATGAAGA TGTTCAGGAG GCTCTGCTCC AGATCATACA 2160
AATGCGGCAG GGGCTTGTGT GCTAGCCGTT AGCACTGACT GCCAGTATCT GTTTTATCTT 2220
GCTGGTGCTG AACATTCTTT GTGCAACTCC ATGGTCTTTC TGGGCCTTAC TGTGCTGGTA 2280
TAATTAAAAT AAAATATATT TTGTTCTAAA AAAAAAAAAA AA 2322

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Lys Asn His Tyr Val Pro Leu Lys Val Ser Glu Asp Met Lys Lys
1 5 10 15
Ser His Asp Ala Ile Ile Asp Asp Leu Asn Arg Lys Leu Leu Asp Val
20 25 30
Thr Gln Lys Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Leu
35 40 45
Glu Asn Asp Ser Leu Ser Lys Asp Val Ser Arg Leu Glu Thr Val Phe
50 55 60
Val Pro Pro Glu Lys His Glu Lys Glu Ile Ile Ala Leu Lys Ser Asn
65 70 75 80
Ile Val Glu Leu Lys Lys Gln Leu Ser Glu Leu Lys Lys Lys Cys Gly
85 90 95
Glu Asp Gln Glu Lys Ile His Ala Leu Thr Ser Glu Asn Thr Asn Leu
100 105 110
Lys Lys Met Met Ser Asn Gln Tyr Val Pro Val Lys Thr His Glu Glu
115 120 125
Val Lys Met Thr Leu Asn Asp Thr Leu Ala Lys Thr Asn Arg Glu Leu
130 135 140
Leu Asp Val Lys Lys Lys Phe Glu Asp Ile Asn Gln Glu Phe Val Lys
145 150 155 160

Ile Lys Asp Lys Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln
 165 170 175
 Asn Gln Ile Lys Ala Glu Tyr Ile Ser Leu Ala Glu His Glu Ala Lys
 180 185 190
 Met Ser Ser Leu Ser Gln Ser Met Arg Lys Val Gln Asp Ser Asn Ala
 195 200 205
 Glu Ile Leu Ala Asn Tyr Arg Lys Gly Gln Glu Glu Ile Val Thr Leu
 210 215 220
 His Ala Glu Ile Lys Ala Gln Lys Lys Glu Leu Asp Thr Ile Gln Glu
 225 230 235 240
 Cys Ile Lys Val Lys Tyr Ala Pro Ile Val Ser Phe Glu Glu Cys Glu
 245 250 255
 Arg Lys Phe Lys Ala Thr Glu Lys Glu Leu Lys Asp Gln Leu Ser Glu
 260 265 270
 Gln Thr Gln Lys Tyr Ser Val Ser Glu Glu Glu Val Lys Lys Asn Lys
 275 280 285
 Gln Glu Asn Asp Lys Leu Lys Lys Glu Ile Phe Thr Leu Gln Lys Asp
 290 295 300
 Leu Arg Asp Lys Thr Val Leu Ile Glu Lys Ser His Glu Met Glu Arg
 305 310 315 320
 Ala Leu Ser Arg Lys Thr Asp Glu Leu Asn Lys Gln Leu Lys Asp Leu
 325 330 335
 Ser Gln Lys Tyr Thr Glu Val Lys Asn Val Lys Glu Lys Leu Val Glu
 340 345 350
 Glu Asn Ala Lys Gln Thr Ser Glu Ile Leu Ala Val Gln Asn Leu Leu
 355 360 365
 Gln Lys Gln His Val Pro Leu Glu Gln Val Glu Ala Leu Lys Lys Ser
 370 375 380
 Leu Asn Gly Thr Ile Glu Asn Leu Lys Glu Glu Leu Lys Ser Met Gln
 385 390 395 400
 Arg Cys Tyr Glu Lys Glu Gln Gln Thr Val Thr Lys Leu His Gln Leu
 405 410 415
 Leu Glu Asn Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln
 420 425 430
 Ile Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu
 435 440 445
 Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Met Glu Glu Val Ser Lys
 450 455 460

Leu Gln Ser Glu Val Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu
 465 470 475 480
 Thr Arg Glu Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp
 485 490 495
 Leu Glu Thr Gln Ile Ser Ser Leu Asn Glu Lys Leu Ala Asn Leu Asn
 500 505 510
 Arg Lys Tyr Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys
 515 520 525
 Glu Ile Ser Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu
 530 535 540
 Gln Glu Ile Lys Asp Gln Lys Glu Arg Cys Asp Lys Ser Leu Thr Thr
 545 550 555 560
 Ile Thr Glu Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu
 565 570 575
 Ala Lys Asp Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu
 580 585 590
 Lys Gln Ala Leu Asn Gly Leu Ser Gln Leu Thr Tyr Thr Ser Gly Asn
 595 600 605
 Pro Thr Lys Arg Gln Ser Gln Leu Ile Asp Thr Leu Gln His Gln Val
 610 615 620
 Lys Ser Leu Glu Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu
 625 630 635 640
 Val Ile Ala Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His
 645 650 655
 Met Asp Glu Asp Val Gln Glu Ala Leu Leu Gln Ile Ile Gln Met Arg
 660 665 670
 Gln Gly Leu Val Cys
 675

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TCTCCCCCT CCCGACACA CACTCACAGG CCGGGCATTG ATGGTAATGT ATGCGAGGAA

60

ACAGCAGAGA CTCAGTGATG GCTGTCACGA CCGGAGGGGG GACTCGCAGC CTTACCAGGC	120
ACTTAAGTAT TCATCGAAGA GTCACCCAG TAGCGGTGAT CACAGACATG AAAAGATGCG	180
AGACGCCGGA GATCCTTCAC CACCAAATAA AATGTTGCGG AGATCTGATA GTCCTGAAAA	240
CAAATACAGT GACAGCACAG GTCACAGTAA GGCCAAAAAT GTGCATACTC ACAGAGTTAG	300
AGAGAGGGAT GGTGGGACCA GTTACTCTCC ACAAGAAAAT TCACACAACC ACAGTGCTCT	360
TCATAGTTCA AATTCACATT CTTCTAATCC AAGCAATAAC CCAAGCAAAA CTTCAGATGC	420
ACCTTATGAT TCTGCAGATG ACTGGTCTGA GCATATTAGC TCTTCTGGGA AAAAGTACTA	480
CTACAATTGT CGAACAGAAG TTTCACAATG GGAAAAACCA AAAGAGTGGC TTGAAAGAGA	540
ACAGAGACAA AAAGAAGCAA ACAAGATGGC AGTCAACAGC TTCCCAAAAG ATAGGGATTA	600
CAGAAGAGAG GTGATGCAAG CAACAGCCAC TAGTGGGTTT GCCAGTGGAA AATCTACATC	660
AGGAGACAAA CCCGTATCAC ATTCTTGCAC AACTCCTTCC ACGTCTTCTG CCTCTGGACT	720
GAACCCCA TCTGCACCTC CAACATCTGC TTCAGCGGTC CCTGTTTCTC CTGTTCCACA	780
GTCGCCAATA CCTCCCTTAC TTCAGGACCC AAATCTTCTT AGACAATTGC TTCCTGCTTT	840
GCAAGCCACG CTGCAGCTTA ATAATTCTAA TGTGGACATA TCTAAAATAA ATGAAGTTCT	900
TACAGCAGCT GTGACACAAG CCTCACTGCA GTCTATAATT CATAAGTTTC TTAGTGCTGG	960
ACCATCTGCT TTCAACATAA CGTCTCTGAT TTCTCAAGCT GCTCAGCTCT CTACACAAGC	1020
CCAGCCATCT AATCAGTCTC CGATGTCTTT AACATCTGAT GCGTCATCCC CAAGATCATA	1080
TGTTTCTCCA AGAATAAGCA CACCTCAAAC TAACACAGTC CCTATCAAAC CTTTGATCAG	1140
TACTCCTCCT GTTTCATCAC AGCCAAAGGT TAGTACTCCA GTAGTTAAGC AAGGACCAGT	1200
GTCACAGTCA GCCACACAGC AGCCTGTAAC TGCTGACAAG CAGCAAGGTC ATGAACCTGT	1260
CTCTCCTCGA AGTCTTCAGC GCTCAAGCCA GAGAAGTCCA TCACCTGGTC CCAATCATAC	1320
TTCTAATAGT AGTAATGCAT CAAATGCAAC AGTTGTACCA CAGAATTCTT CTGCCCCGATC	1380
CACGTGTTCA TTAACGCCTG CACTAGCAGC AACTTTCAGT GAAAATCTCA TAAACACGT	1440
TCAAGGATGG CCTGCAGATC ATGCAGAGAA GCAGGCATCA AGATTACGCG AAGAAGCGCA	1500
TAACATGGGA ACTATTCACA TGTCCGAAAT TTGTACTGAA TTAAAAAATT TAAGATCTTT	1560
AGTCCGAGTA TGTGAAATTC AAGCAACTTT GCGAGAGCAA AGGATACTAT TTTTGAGACA	1620
ACAAATTAAG GAACTTGAAA AGCTAAAAAA TCAGAATTCC TTCATGGTGT GAAGATGTGA	1680
ATAATTGCAC ATGGTTTTGA GAACAGGAAC TGTAATCTG TTGCCCAATC TTAACATTTT	1740

TGAGCTGCAT TTAAGTAGAC TTTGGACCGT TAAGCTGGGC AAAGGAAATG ACAAGGGGAC 1800
GGGGTCTGTG AGAGTCAATT CAGGGGAAAG ATACAAGATT GATTTGTAAA ACCCTTGAAA 1860
TGTAGATTTT TTGTAGATGT ATCCTTCACG TTGTAAATAT GTTTTGTAGA GTGAAGCCAT 1920
GGGAAGCCAT GTGTAACAGA GCTTAGACAT CCAAACTAA TCAATGCTGA GGTGGCTAAA 1980
TACCTAGCCT TTTACATGTA AACCTGTCTG CAAAATTAGC TTTTAAATAA AAAAAAAAAA 2040
A 2041

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Arg Gly Asn Ser Arg Asp Ser Val Met Ala Val Thr Thr Gly Gly
1 5 10 15
Gly Thr Arg Ser Leu Thr Arg His Leu Ser Ile His Arg Arg Val Thr
20 25 30
Pro Val Ala Val Ile Thr Asp Met Lys Arg Cys Glu Thr Pro Glu Ile
35 40 45
Leu His His Gln Ile Lys Cys Cys Gly Asp Leu Ile Val Leu Lys Thr
50 55 60
Asn Thr Val Thr Ala Gln Val Thr Val Arg Pro Lys Met Cys Ile Leu
65 70 75 80
Thr Glu Leu Glu Arg Gly Met Val Gly Pro Val Thr Leu His Lys Lys
85 90 95
Ile His Thr Thr Thr Val Leu Phe Ile Val Gln Ile His Ile Leu Leu
100 105 110
Ile Gln Ala Ile Thr Gln Ala Lys Leu Gln Met His Leu Met Ile Leu
115 120 125
Gln Met Thr Gly Leu Ser Ile Leu Ala Leu Leu Gly Lys Ser Thr Thr
130 135 140
Thr Ile Val Glu Gln Lys Phe His Asn Gly Lys Asn Gln Lys Ser Gly
145 150 155 160
Leu Lys Glu Asn Arg Asp Lys Lys Lys Gln Thr Arg Trp Gln Ser Thr

Ala Ser Gln Lys Ile Gly Ile Thr Glu Glu Arg
180 185

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GCCCTATCCA CTTAATAGAT GCCAATTCAA AGAGGTTAAA TGATTAGACT AAGGCACCTA	60
ACTTATGTGA GTGTCAGGCT TCAATGCCTG TGTTAGAGCT ACTCCTTCAC ACAAATAGT	120
TCAGAACATA GAGAAGGACC AAGGTTAATA AATGATTTTC ATCCCAAACA CTAAACATGA	180
TTGATGGGTA GAGGCTGCCC GAAGTACTGT GTAAAGATGG AATCTGAGAT AGAAGAATGC	240
TGTGGTCAAT TAGTAATTCT TGCCCATGGA GGGATTAGTG ACACATGCCT TGTATATTTG	300
TCATCTGTGG CCTAAACTCT GCCCCTGAAG GTTTGTTTTT TAATTCAGAG GTTTAAATTA	360
ATCTAGCCCA CTTAATAAAA CCAGAGATCC TATGGGAAAT TTAGCCTAAG ACAGTGCTGG	420
AAATTGCCAT ATGTTGATAC AAAGAAGTGT TTGGCCACAT TACAGGTCTC AGACTCAACT	480
GCTATGTGTG ACTGCCGCTC TGTGCCTATG TCTTGCTTTT TTGCTGAGTT CCCTATTTCC	540
ATATCTCCAG GTGAATCCAT GAGAAGCGAG AGGGTGGCTG AGAGGCCTGG GCCTCTGGGA	600
TTCCACCTTG CTATCTCTGC TCTTCAACCA TTGTTTTAGA CTCTGAACAC CAGATCCTCA	660
TATCTGAAAG TGATTTGGAG ACCTGGGCAT CAAGTGCTCT TTTAAGAAGG GGCTATCCCA	720
GAGGACTGTT CAAAAGTCTC ATTCAATAGA GATGTTGGAG TCCCAGAACA AAGTTAGGGA	780
GCAAACCAGT AACCTATGCT GGTSGTAACA GAGGATCCTA CAATTACGTT TGTTTTTAAG	840
ACAGGATTTT GCTGTGTTGC CCAGACTGGT CTCAAACCTC TGGGTTCAAG AGATCCATCC	900
TCCCACCTCA GTCTCCTGAA AGCTGGGATG ACAGGCACAT GCCACCACAC CTAGCTCCTT	960
ACAACCATTT ATTTTAACTT ATTTCATTTA TAACTGGTAT CTTTCATTTG TATGTGGCAG	1020
CTAGAGATTT ATATAGGATG GAAGTAATTT ATTTTAAATT TAAATATTTT ATGTTGAACT	1080
GTTTGCCTTG TATGGAACAT TTTACTTGGC CAATTCAAAT AAAAATAAAG TCAGCTTTGT	1140

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Leu	Ile	Gln	Arg	Ser	Val	Trp	Pro	His	Tyr	Arg	Ser	Gln	Thr	Gln
1				5				10					15		
Leu	Leu	Cys	Val	Thr	Ala	Ala	Leu	Cys	Leu	Cys	Leu	Ala	Phe	Leu	Leu
			20				25					30			
Ser	Ser	Leu	Phe	Pro	Tyr	Leu	Gln	Val	Asn	Pro					
		35				40									

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3067 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCGGTGGCTG	AGGCGGCTGG	GCCTAGGGTG	CAGCGGGCGC	GTCTGCGGCT	GGTGTGGCG	60
CATCTCTAGA	TCCTTTCCCG	GAGTTCAGTT	ATGGGTGTGA	GAGGTTTGCA	AGGATTTGTG	120
GGAAGTACCT	GCCCACATAT	ATGTACAGTA	GTAAATTTCA	AAGAACTGGC	AGAGCACCAC	180
CGAAGCAAGT	ATCCTGGATG	TACCCCTACC	ATTGTGGTTG	ATGCCATGTG	TTGTCTCAGA	240
TATTGGTATA	CTCCAGAATC	TTGGATCTGC	GGTGGCCAGT	GCGGAGAATA	CTTTTCTGCT	300
TTGCGAGATT	TTGTTAAAAC	TTTTACGGCA	GCTGGGATCA	AGTTGATATT	CTTCTTTGAT	360
GGCATGGTGG	AGCAGGATAA	GAGAGATGAA	TGGGTGAAAC	GAAGGCTCAA	GAACAACAGG	420
GAGATATCCA	GGATTTTTC	TTACATCAAG	TCACACAAGG	AGCAGCCAGG	CAGAAATATG	480
TTCTTCATCC	CCTCAGGGCT	AGCTGTGTTT	ACACGATTTG	CTCTAAAGAC	ACTGGGCCAG	540
GAACTTTGT	GTTCTTTGCA	GGAAGCAGAT	TATGAGGTAG	CTTCCTATGG	CCTCCAGCAT	600

AACTGTCTTG	GGATTCTGGG	GGAAGACACT	GATTACCTAA	TCTATGACAC	TTGTCCCTAC	660
TTTTCAATTA	GCGAGCTCTG	CCTAGAGAGC	CTGGACACCG	TCATGCTCTG	CAGAGAGAAG	720
CTCTGTGAGA	GTCTGGGCCT	CTGTGTGGCC	GACCTTCCTC	TTCTGGCCTG	CCTCCTTGGC	780
GACGACATAA	TCCCAGAGGG	CATGTTTGAA	AGCTTTAGGT	ACAAATGCTT	ATCGTCCTAC	840
ACCTCTGTAA	AAGAGAACTT	TGACAAAAAA	GGTAACATCA	TATTAGCTGT	GTCAGACCAT	900
ATATCGAAAAG	TTCTTTACTT	GTATCAAGGT	GAGAAAAAAT	TAGAAGAGAT	ATTACCTCTG	960
GGACCAAACA	AAGCTCTTTT	TTATAAAGGA	ATGGCATCAT	ATCTTTTACC	AGGACAAAAA	1020
TCTCCATGGT	TTTTCAAAA	ACCCAAAGGT	GTAATAACTT	TGGACAAACA	AGTAATATCC	1080
ACGAGTTCAG	ACGCCGAATC	CAGGGAAGAA	GTTCCCATGT	G TTCAGATGC	TGAATCCAGG	1140
CAAGAAGTTC	CCATGTGTAC	AGGCCCTGAA	TCCAGGCGAG	AAGTTCCCGT	GTATACAGAT	1200
TCTGAACCCA	GGCAAGAAGT	TCCCATGTGT	TCAGACCCTG	AACCCAGGCA	AGAAGTTCCC	1260
ACATGTACAG	GCCCTGAATC	CAGGCGAGAA	GTTCCCATGT	G TTCAGACCC	TGAACCCAGG	1320
CAAGAAGTTC	CCATGTGTAC	AGGCCCTGAA	GCCAGGCAAG	AAGTTCCCAT	GTATACAGAC	1380
TCTGAACCCA	GGCAAGAAGT	TCCCATGTAT	ACAGACTCTG	AACCCAGGCA	AGAAGTTCCC	1440
ATGTATACAG	GCTCTGAACC	CAGGCAAGAA	GTTCCCATGT	ATACAGGCCC	TGAATCCAGG	1500
CAAGAAGTTC	CCATGTATAC	AGGCCCTGAA	TCCAGGCAAG	AAGTTTTAAT	ACGGACAGAC	1560
CCTGAATCTA	GGCAAGAAAT	TATGTGTACA	GGCCATGAAT	CCAAACAGGA	AGTTCCCAT	1620
TGTACAGATC	CTATATCCAA	GCAAGAAGAC	TCCATGTGTA	CACACGCTGA	AATCAATCAA	1680
AAATTACCTG	TAGCAACAGA	TTTTGAATTT	AAGCTAGAAG	CTCTCATGTG	TACAAACCCT	1740
GAAATTAAAC	AAGAAGACCC	CACAAATGTG	GGGCCTGAAG	TAAAGCAACA	AGTAACCATG	1800
GTTTCAGACA	CTGAAATCTT	AAAGGTTGCT	AGAACACATC	ACGTCCAAGC	AGAAAGCTAC	1860
CTGGTGTACA	ACATCATGAG	CAGTGGAGAG	ATTGAATGCA	GCAACACCCT	AGAAGATGAG	1920
CTTGACCAGG	CCTTACCCAG	CCAGGCCTTC	ATTTACCGTC	CCATTGACA	GCGGGTCTAC	1980
TCACTCTTAC	TGGAGGACTG	TCAAGATGTC	ACCAGCACCT	GCCTAGCTGT	CAAGGAGTGG	2040
TTTGTGTATC	CTGGGAACCC	ACTGAGGCAC	CCGACCTCG	TCAGGCCGCT	GCAGATGACC	2100
ATTCCAGGGG	GAACGCCTAG	TTTGAAAATA	TTATGGCTGA	ACCAAGAGCC	AGAAATACAG	2160
GTTCGGCGCT	TGGACACACT	CCTAGCCTGT	TTCAATCTTT	CCTCCTCAAG	AGAAGAGCTG	2220
CAGGCTGTCTG	AAAGCCCATT	TCAAGCTTTG	TGCTGCCTCT	TGATCTACCT	CTTTGTCCAG	2280

GTGGACACGC TTTGCCTGGA GGATTTGCAT GCGTTTATTG CGCAGGCCTT GTGCCTCCAA 2340
GGAAAATCCA CCTCGCAGCT TGTAATCTA CAGCCTGATT ACATCAACCC CAGAGCCGTG 2400
CAGCTGGGCT CCCTTCTCGT CCGCGGCCTC ACCACTCTGG TTTTAGTCAA CAGCGCATGT 2460
GGCTTCCCTT GGAAGACGAG TGATTTTCATG CCCTGGAATG TATTTGACGG GAAGCTTTTT 2520
CATCAGAAGT ACTTGCAATC TGAAAAGGGT TATGCTGTGG AGGTTCTTTT AGAACAAAAT 2580
GGAGGTGGGG AAGACAGGGC TCCAGCTACC ACAGGACGGG CTCTGGGTAT AGCCGTTCCA 2640
GTCAGGGACA GCCGTGGAGA GACCAGGGAC CAGGAAGCAG ACAGTATGAG CATGACCAGT 2700
GGAGAAGGTA CTAGTCAACC TCCAGAAAGA GTATGGAGAG AAAAAGAGGC ACACCTGGAC 2760
GCAGAGCCCT GCCAGCGCCC TCCTCTGCTG TTGCAGCTGC AAGGAGACCA TGCCTGTGGG 2820
AGCCAGGCCT CGCTTGCATG AAGAAGGAAC GATGCCTTTT TCAATGGTGT CTCCCTCCCA 2880
TTGTGCAGAA GAGCTTTTGT TGGCTTCTCT CCCGAGCTTG TGCCTGATTC TGTGGCCCAA 2940
AACAATCATT GTTAACATCT TCATGTGTTT CATTCTGATC TTTCATTCAT ATATATGATG 3000
CCTAGCTAAT TTCATTTTAA AATAAATGGG AATCTGTTGT AAAAAAAAAA AAAAAAAAAA 3060
AAAAAAA 3067

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	Gly	Val	Arg	Gly	Leu	Gln	Gly	Phe	Val	Gly	Ser	Thr	Cys	Pro	His
1				5				10					15		
Ile	Cys	Thr	Val	Val	Asn	Phe	Lys	Glu	Leu	Ala	Glu	His	His	Arg	Ser
			20					25					30		
Lys	Tyr	Pro	Gly	Cys	Thr	Pro	Thr	Ile	Val	Val	Asp	Ala	Met	Cys	Cys
			35					40					45		
Leu	Arg	Tyr	Trp	Tyr	Thr	Pro	Glu	Ser	Trp	Ile	Cys	Gly	Gly	Gln	Trp
			50				55				60				
Arg	Glu	Tyr	Phe	Ser	Ala	Leu	Arg	Asp	Phe	Val	Lys	Thr	Phe	Thr	Ala
						70				75					80

Ala	Gly	Ile	Lys	Leu	Ile	Phe	Phe	Phe	Asp	Gly	Met	Val	Glu	Gln	Asp	
				85					90						95	
Lys	Arg	Asp	Glu	Trp	Val	Lys	Arg	Arg	Leu	Lys	Asn	Asn	Arg	Glu	Ile	
			100					105						110		
Ser	Arg	Ile	Phe	His	Tyr	Ile	Lys	Ser	His	Lys	Glu	Gln	Pro	Gly	Arg	
		115					120					125				
Asn	Met	Phe	Phe	Ile	Pro	Ser	Gly	Leu	Ala	Val	Phe	Thr	Arg	Phe	Ala	
	130						135					140				
Leu	Lys	Thr	Leu	Gly	Gln	Glu	Thr	Leu	Cys	Ser	Leu	Gln	Glu	Ala	Asp	
145					150					155					160	
Tyr	Glu	Val	Ala	Ser	Tyr	Gly	Leu	Gln	His	Asn	Cys	Leu	Gly	Ile	Leu	
				165					170					175		
Gly	Glu	Asp	Thr	Asp	Tyr	Leu	Ile	Tyr	Asp	Thr	Cys	Pro	Tyr	Phe	Ser	
			180					185						190		
Ile	Ser	Glu	Leu	Cys	Leu	Glu	Ser	Leu	Asp	Thr	Val	Met	Leu	Cys	Arg	
		195					200					205				
Glu	Lys	Leu	Cys	Glu	Ser	Leu	Gly	Leu	Cys	Val	Ala	Asp	Leu	Pro	Leu	
	210					215					220					
Leu	Ala	Cys	Leu	Leu	Gly	Asp	Asp	Ile	Ile	Pro	Glu	Gly	Met	Phe	Glu	
225					230					235					240	
Ser	Phe	Arg	Tyr	Lys	Cys	Leu	Ser	Ser	Tyr	Thr	Ser	Val	Lys	Glu	Asn	
			245						250					255		
Phe	Asp	Lys	Lys	Gly	Asn	Ile	Ile	Leu	Ala	Val	Ser	Asp	His	Ile	Ser	
			260					265						270		
Lys	Val	Leu	Tyr	Leu	Tyr	Gln	Gly	Glu	Lys	Lys	Leu	Glu	Glu	Ile	Leu	
		275					280					285				
Pro	Leu	Gly	Pro	Asn	Lys	Ala	Leu	Phe	Tyr	Lys	Gly	Met	Ala	Ser	Tyr	
	290					295					300					
Leu	Leu	Pro	Gly	Gln	Lys	Ser	Pro	Trp	Phe	Phe	Gln	Lys	Pro	Lys	Gly	
305					310					315					320	
Val	Ile	Thr	Leu	Asp	Lys	Gln	Val	Ile	Ser	Thr	Ser	Ser	Asp	Ala	Glu	
				325					330					335		
Ser	Arg	Glu	Glu	Val	Pro	Met	Cys	Ser	Asp	Ala	Glu	Ser	Arg	Gln	Glu	
			340					345					350			
Val	Pro	Met	Cys	Thr	Gly	Pro	Glu	Ser	Arg	Arg	Glu	Val	Pro	Val	Tyr	
		355					360					365				
Thr	Asp	Ser	Glu	Pro	Arg	Gln	Glu	Val	Pro	Met	Cys	Ser	Asp	Pro	Glu	
	370					375					380					

Pro Arg Gln Glu Val	Pro Thr Cys Thr Gly	Pro Glu Ser Arg Arg Glu
385	390	395 400
Val Pro Met Cys Ser Asp	Pro Glu Pro Arg Gln Glu Val	Pro Met Cys
405	410	415
Thr Gly Pro Glu Ala Arg Gln Glu Val	Pro Met Tyr Thr Asp Ser Glu	
420	425	430
Pro Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu	Pro Arg Gln Glu	
435	440	445
Val Pro Met Tyr Thr Gly Ser Glu Pro Arg Gln Glu Val	Pro Met Tyr	
450	455	460
Thr Gly Pro Glu Ser Arg Gln Glu Val Pro Met Tyr Thr Gly Pro Glu		
465	470	475 480
Ser Arg Gln Glu Val Leu Ile Arg Thr Asp Pro Glu Ser Arg Gln Glu		
485	490	495
Ile Met Cys Thr Gly His Glu Ser Lys Gln Glu Val Pro Ile Cys Thr		
500	505	510
Asp Pro Ile Ser Lys Gln Glu Asp Ser Met Cys Thr His Ala Glu Ile		
515	520	525
Asn Gln Lys Leu Pro Val Ala Thr Asp Phe Glu Phe Lys Leu Glu Ala		
530	535	540
Leu Met Cys Thr Asn Pro Glu Ile Lys Gln Glu Asp Pro Thr Asn Val		
545	550	555 560
Gly Pro Glu Val Lys Gln Gln Val Thr Met Val Ser Asp Thr Glu Ile		
565	570	575
Leu Lys Val Ala Arg Thr His His Val Gln Ala Glu Ser Tyr Leu Val		
580	585	590
Tyr Asn Ile Met Ser Ser Gly Glu Ile Glu Cys Ser Asn Thr Leu Glu		
595	600	605
Asp Glu Leu Asp Gln Ala Leu Pro Ser Gln Ala Phe Ile Tyr Arg Pro		
610	615	620
Ile Arg Gln Arg Val Tyr Ser Leu Leu Leu Glu Asp Cys Gln Asp Val		
625	630	635 640
Thr Ser Thr Cys Leu Ala Val Lys Glu Trp Phe Val Tyr Pro Gly Asn		
645	650	655
Pro Leu Arg His Pro Asp Leu Val Arg Pro Leu Gln Met Thr Ile Pro		
660	665	670
Gly Gly Thr Pro Ser Leu Lys Ile Leu Trp Leu Asn Gln Glu Pro Glu		
675	680	685

Ile	Gln	Val	Arg	Arg	Leu	Asp	Thr	Leu	Leu	Ala	Cys	Phe	Asn	Leu	Ser	690	695	700	
Ser	Ser	Arg	Glu	Glu	Leu	Gln	Ala	Val	Glu	Ser	Pro	Phe	Gln	Ala	Leu	705	710	715	720
Cys	Cys	Leu	Leu	Ile	Tyr	Leu	Phe	Val	Gln	Val	Asp	Thr	Leu	Cys	Leu	725	730	735	
Glu	Asp	Leu	His	Ala	Phe	Ile	Ala	Gln	Ala	Leu	Cys	Leu	Gln	Gly	Lys	740	745	750	
Ser	Thr	Ser	Gln	Leu	Val	Asn	Leu	Gln	Pro	Asp	Tyr	Ile	Asn	Pro	Arg	755	760	765	
Ala	Val	Gln	Leu	Gly	Ser	Leu	Leu	Val	Arg	Gly	Leu	Thr	Thr	Leu	Val	770	775	780	
Leu	Val	Asn	Ser	Ala	Cys	Gly	Phe	Pro	Trp	Lys	Thr	Ser	Asp	Phe	Met	785	790	795	800
Pro	Trp	Asn	Val	Phe	Asp	Gly	Lys	Leu	Phe	His	Gln	Lys	Tyr	Leu	Gln	805	810	815	
Ser	Glu	Lys	Gly	Tyr	Ala	Val	Glu	Val	Leu	Leu	Glu	Gln	Asn	Gly	Gly	820	825	830	
Gly	Glu	Asp	Arg	Ala	Pro	Ala	Thr	Thr	Gly	Arg	Ala	Leu	Gly	Ile	Ala	835	840	845	
Val	Pro	Val	Arg	Asp	Ser	Arg	Gly	Glu	Thr	Arg	Asp	Gln	Glu	Ala	Asp	850	855	860	
Ser	Met	Ser	Met	Thr	Ser	Gly	Glu	Gly	Thr	Ser	Gln	Pro	Pro	Glu	Arg	865	870	875	880
Val	Trp	Arg	Glu	Lys	Glu	Ala	His	Leu	Asp	Ala	Glu	Pro	Cys	Gln	Arg	885	890	895	
Pro	Pro	Leu	Leu	Leu	Gln	Leu	Gln	Gly	Asp	His	Ala	Cys	Gly	Ser	Gln	900	905	910	
Ala	Ser	Leu	Ala													915			

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGCTGTCTGC TCTCCTGGCA GGAATCGCTG AGGGAGGGAA ACGCGGCTCT GAATCAGCCC	60
AGAACGAGCC TTCGGAAGC TCACCCTCCG ATCTCGGTGT GATTGTTGTG ATTGTTGTGA	120
TTTCCTGTCT CGTTTGCCTT GACCGCCATG TGAAAGAATC TGTTCCCCAG CTAGGTGGGG	180
AAAATTCACA GGTGGGCTGT CTGTAGAGAG AACTGGCTGA TTAAAGGCTT CTCGTCCCGA	240
TTTTGTGATA GCCAAGTGCT TGGCCTGGTC GACGGTCTTT GCTCCTTTAC AAATAAAGTG	300
TTCTGTTTCA GTTCGTCCCA AGTTTTCCAT GAAGGGCAGT GGTTCCCTGA CCTCCCAGGT	360
GCCTGGGCTT CCCAGGTTT CTGATCTGGG GCTTGGGGCC CTGTGTTTGG GGATCGTGGC	420
ACTGTGTGCA CCAGCCTGGA AGCACTGGGC CAGTCTTGGC CAAGCTTTCC ATCAGGGATG	480
ATTTGATCTT GGTGCTACAG GTCTGTGGTA CGACCATTGT TCCACACCAC ATGTCATTAA	540
TAATGCTTCC CATGCTTCTG CTTGCAAATG ACCAGCCTTC CAAACAGCCA GAGCTGTTTC	600
GAGGTGTTTC TGCAGGCAGG TGCAGGCGTG CCCTCAAATA AGCTTTGCCA ATGGAGTCTC	660
AGCAAGAGCA AAACCTGGTC AGGAAAGACA AAGCCTGGGA ATCCACCCCC ATGCCCTGCA	720
GGTTGGCTGG CCCTGGAGCC ATTTATTATA GTGCTAATCA TGTTTCTAGG CAGGTGCAGA	780
TGGCAAGGGC AGTGTCTTGG TGAGCTTTTT AGCACGAAGA GCCAGGTCTG TCGAAGCCTT	840
TGTGAGAGCT GGAAACGCAG GTGTGCTGGG CATGCGCAGT ATGGGGTTTC GGGCTCAGGG	900
CTTGCCCTTT GGCATCAGAC AGACCTGGCT TCGCATCCTG GATTGCTTC TGACGTGCAC	960
CCTTCCCTTT GGGTCTCGTG ATGTGAAATG GAGATGTTGT CATTTGTGAG GGCTCCATGA	1020
AGTTTCGTTG AAATGACAAA TACTAATTTT TTCATCTGTG AAATGGAGAT AATAGTGCTG	1080
ACCTCAGAAC AGCTGAGAGG ACTAAATGAA ATGATGTTGG ATGTAGCCAT AAAGAACGAA	1140
GTCAGGCACT GGTGCACGCC TGGAATCCCA GCTCTTGGGA GACCGAGACA GGTGGATTGC	1200
TTGAGCTCAG GAGTTTGAGA CCAGCCTGAG CAACATAGGG AGGTCCAGTC TCTACAAAAA	1260
ATATGAAAAG TAGCTGGGCG TGGTGGCGCA TGCCTGTAGT CCCACTACTT GGAAGGCTTC	1320
GTTGGGAGGA TCACTTGAGC CCAGAAGATT GAGGCTGCAG TAAGCCGTGA TCGTGCCACT	1380
GCATTCCAGC CTGGGCAACA GAGCGAGACA CTGTCTCAAA TAAAAAAGAT GGGAATAGTA	1440
GACACTGGGG GCTCCAGAAG GAGGGAGGGA GGGAGGAAGG GGAGGAAGGG CTGAAATGCT	1500
TTCTATTGGA TACTATCTGG GCATATTACT TCCTGTGGTT CACTGTCTGG GTGACAGGAT	1560
TCATAGAAGC CCAAACTTTA GCACCACGCA GCATACCTTT GTAACAAAGC CGCACACGTA	1620
CGCCCTCAAG CTAAAACAAA AGTGGACCGG GAGGCCGAGG TCGGGGGATC ATGAGGTCAG	1680

GAGTTTGAGA CCAGCCTGGC AGATAACGGT GAAACCCCGT CTCTACTAAA AATACCAAAA 1740
AAAGTTAGCC GGACATGGTG GCAGGTGCCT GTAGTCCCAG CTACTTGGGA GGCTGGGGCA 1800
GAAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATTGC GCCACTGCAC 1860
TCCAGCCTGT GCGACAGAGT GAGACTCCGT CTCAAAAAAA AAAAAAAAAA AAAA 1914

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Thr	Ser	Leu	Pro	Asn	Ser	Gln	Ser	Cys	Phe	Glu	Val	Phe	Leu	Gln	1	5	10	15
Ala	Gly	Ala	Gly	Val	Pro	Ser	Asn	Lys	Leu	Cys	Gln	Trp	Ser	Leu	Ser	20	25	30	
Lys	Ser	Lys	Thr	Trp	Ser	Gly	Lys	Thr	Lys	Pro	Gly	Asn	Pro	Pro	Pro	35	40	45	
Cys	Pro	Ala	Gly	Trp	Leu	Ala	Leu	Glu	Pro	Phe	Ile	Ile	Val	Leu	Ile	50	55	60	
Met	Phe	Leu	Gly	Arg	Cys	Arg	Trp	Gln	Gly	Gln	Cys	Leu	Gly	Glu	Leu	65	70	75	80
Phe	Ser	Thr	Lys	Ser	Gln	Val	Cys	Arg	Ser	Leu	Cys	Glu	Ser	Trp	Lys	85	90	95	
Arg	Arg	Cys	Ala	Gly	His	Ala	Gln	Tyr	Gly	Val	Ser	Gly	Ser	Gly	Leu	100	105	110	
Ala	Leu	Trp	His	Gln	Thr	Asp	Leu	Ala	Ser	His	Pro	Gly	Phe	Ala	Ser	115	120	125	
Asp	Val	His	Pro	Ser	Leu	Trp	Val	Ser	130	135									

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 575 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC      60
ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC      120
CATTCCGCTG TGTTGATTGA GGACGTTCCTT TTCACGGAGA AAGATTTTGA GAATGGCCCC      180
CAGAACATAT ACAACCTTTA CGAGCAAGTC AGCTACAACCT GTTTCATCGC TGCAGGCCTT      240
TACCTCCTCC TCGGAGGCTT CTCTTTCTGC CAAGTTCGGC TCAATAAGCG CAAGGAATAC      300
ATGGTGCGCT AGGGCCCCGG CGCGTTTCCC CGCTCCAGCC CCTCCTCTAT TTAAAGACTC      360
CCTGCACCGT GTCACCCAGG TCGCGTCCCA CCCTTGCCGG CGCCCTCTGT GGGACTGGGT      420
TTCCCGGGCG AGAGACTGAA TCCCTTCTCC CATCTCTGGC ATCCGGCCCC CGTGGAGAGG      480
GCTGAGGCTG GGGGGCTGTT CCGTCTCTCC ACCCTTCGCT GTGTCCCGTA TCTCAATAAA      540
GAGAATCTGC TCTCTTCAAA AAAAAAAAAA AAAAAA      575
```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
1           5           10           15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
20          25          30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
35          40          45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
```

Val Arg

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GNAGCCCAGGA GTCTTCTCAA CCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ANCAGTCGCAA GTGCATAGTA ACCCAGTA

29

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TNCTCAGCTTT TATTTGGTTC TGAGTGTT

29

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TNTGCTCAGAC CAGTCATCTG CAGAATCA

29

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

TNCAGCACTGT CTTAGGCTAA ATTTCCCA

29

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GNATTCGGCGT CTGAACTCGT GGATATTA

29

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ANATGCCCGAGA TAGTATCCAA TAGAAAGC

29

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CNACAGCACAG GAGCGACGCC ATAAAGAA

29

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Val Met Tyr Ala Arg Lys Gln Gln Arg Leu Ser Asp Gly Cys His
1 .5 10 15
Asp Arg Arg Gly Asp Ser Gln Pro Tyr Gln Ala Leu Lys Tyr Ser Ser
20 25 30
Lys Ser His Pro Ser Ser Gly Asp His Arg His Glu Lys Met Arg Asp
35 40 45
Ala Gly Asp Pro Ser Pro Pro Asn Lys Met Leu Arg Arg Ser Asp Ser
50 55 60
Pro Glu Asn Lys Tyr Ser Asp Ser Thr Gly His Ser Lys Ala Lys Asn
65 70 75 80
Val His Thr His Arg Val Arg Glu Arg Asp Gly Gly Thr Ser Tyr Ser
85 90 95

Pro Gln Glu Asn Ser His Asn His Ser Ala Leu His Ser Ser Asn Ser
 100 105 110
 His Ser Ser Asn Pro Ser Asn Asn Pro Ser Lys Thr Ser Asp Ala Pro
 115 120 125
 Tyr Asp Ser Ala Asp Asp Trp Ser Glu His Ile Ser Ser Ser Gly Lys
 130 135 140
 Lys Tyr Tyr Tyr Asn Cys Arg Thr Glu Val Ser Gln Trp Glu Lys Pro
 145 150 155 160
 Lys Glu Trp Leu Glu Arg Glu Gln Arg Gln Lys Glu Ala Asn Lys Met
 165 170 175
 Ala Val Asn Ser Phe Pro Lys Asp Arg Asp Tyr Arg Arg Glu Val Met
 180 185 190
 Gln Ala Thr Ala Thr Ser Gly Phe Ala Ser Gly Lys Ser Thr Ser Gly
 195 200 205
 Asp Lys Pro Val Ser His Ser Cys Thr Thr Pro Ser Thr Ser Ser Ala
 210 215 220
 Ser Gly Leu Asn Pro Thr Ser Ala Pro Pro Thr Ser Ala Ser Ala Val
 225 230 235 240
 Pro Val Ser Pro Val Pro Gln Ser Pro Ile Pro Pro Leu Leu Gln Asp
 245 250 255
 Pro Asn Leu Leu Arg Gln Leu Leu Pro Ala Leu Gln Ala Thr Leu Gln
 260 265 270
 Leu Asn Asn Ser Asn Val Asp Ile Ser Lys Ile Asn Glu Val Leu Thr
 275 280 285
 Ala Ala Val Thr Gln Ala Ser Leu Gln Ser Ile Ile His Lys Phe Leu
 290 295 300
 Thr Ala Gly Pro Ser Ala Phe Asn Ile Thr Ser Leu Ile Ser Gln Ala
 305 310 315 320
 Ala Gln Leu Ser Thr Gln Ala Gln Pro Ser Asn Gln Ser Pro Met Ser
 325 330 335
 Leu Thr Ser Asp Ala Ser Ser Pro Arg Ser Tyr Val Ser Pro Arg Ile
 340 345 350
 Ser Thr Pro Gln Thr Asn Thr Val Pro Ile Lys Pro Leu Ile Ser Thr
 355 360 365
 Pro Pro Val Ser Ser Gln Pro Lys Val Ser Thr Pro Val Val Lys Gln
 370 375 380
 Gly Pro Val Ser Gln Ser Ala Thr Gln Gln Pro Val Thr Ala Asp Lys
 385 390 395 400
 Gln Gln Gly His Glu Pro Val Ser Pro Arg Ser Leu Gln Arg Ser Ser

				405						410						415
Gln	Arg	Ser	Pro	Ser	Pro	Gly	Pro	Asn	His	Thr	Ser	Asn	Ser	Ser	Asn	
			420					425					430			
Ala	Ser	Asn	Ala	Thr	Val	Val	Pro	Gln	Asn	Ser	Ser	Ala	Arg	Ser	Thr	
		435					440					445				
Cys	Ser	Leu	Thr	Pro	Ala	Leu	Ala	Ala	His	Phe	Ser	Glu	Asn	Leu	Ile	
	450					455					460					
Lys	His	Val	Gln	Gly	Trp	Pro	Ala	Asp	His	Ala	Glu	Lys	Gln	Ala	Ser	
465				470					475						480	
Arg	Leu	Arg	Glu	Glu	Ala	His	Asn	Met	Gly	Thr	Ile	His	Met	Ser	Glu	
			485						490						495	
Ile	Cys	Thr	Glu	Leu	Lys	Asn	Leu	Arg	Ser	Leu	Val	Arg	Val	Cys	Glu	
		500						505					510			
Ile	Gln	Ala	Thr	Leu	Arg	Glu	Gln	Arg	Ile	Leu	Phe	Leu	Arg	Gln	Gln	
	515						520						525			
Ile	Lys	Glu	Leu	Glu	Lys	Leu	Lys	Asn	Gln	Asn	Ser	Phe	Met	Val		
	530					535					540					

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CAGTGGAGTC TGTACTGGCT GCGGGGGACC CTGCTCATTT GAAAATCTGA CATCAGCTGG	60
GCAGTCGCCC CCCTCCTCCT TTCCTCCCTC TACTCTGACA CAGCACTTAG CACCTGAATC	120
TTCGTTTCTC TCCCAGGGAC CCTCCATTTT CCATATCCAG GAAAATGTGA TGCGCCACAG	180
GTATCAGCGT CTGGATCGCC ACTTCACGTT TTAGCCACAA GTGACTCAGT GGAAGATCCA	240
GAGTCAACAG AGGCTCGTCA GGAAGATGTC TACAGAAAAG GTAGACCAA AGGAGGAAGC	300
TGGGGAAAAA GAGGTGTGCG GAGACCAGAT CAARGGACCG GACAAAGAGG AGGAACCACC	360
AGCTGCTGCA TCCCATGGCC AGGGGTGGCG TCCAGGTGGC AGAGCAGCTA GGAACGCAAG	420
GCCTGAACCT GGGGCCAGAC ACCCTGCTCT CCCGGCCATG GTCAACGACC CTCCAGTACC	480
TGCCTTACTG TGGGCCCAGG AGGTGGGCCA AGTCTTGGCA GGCCGTGCCC GCAGGCTGCT	540

GCTGCAGTTT GGGGTGCTCT TCTGCACCAT CCTCCTTTTG CTCTGGGTGT CTGTCTTCCT	600
CTATGGCTCC TTCTACTATT CCTATATGCC GACAGTCAGC CACCTCAGCC CTGTGCATTT	660
CTACTACAGG ACCGACTGTG ATTCCTCCAC CACCTCACTC TGCTCCTTCC CTGTTGCCAA	720
TGTCTCGCTG ACTAAGGGTG GACGTGATCG GGTGCTGATG TATGGACAGC CGTATCGTGT	780
TACCTTAGAG CTTGAGCTGC CAGAGTCCCC TGTGAATCAA GATTGGGGCA TGTTCTTGGT	840
CACCATTTCC TGCTACACCA GAGGTGGCCG AATCATCTCC ACTTCTTCGC GTTCGGTGAT	900
GCTGCATTAC CGCTCAGACC TGCTCCAGAT GCTGGACACA CTGGTCTTCT CTAGCCTCCT	960
GCTATTTGGC TTTGCAGAGC AGAAGCAGCT GCTGGAGGTG GAACTCTACG CAGACTATAG	1020
AGAGAACTCG TACGTGCCGA CCACTGGAGC GATCATTGAG ATCCACAGCA AGCGCATCCA	1080
GCTGTATGGA GCCTACCTCC GCATCCACGC GCACTTCACT GGGCTCAGAT ACCTGCTATA	1140
CAACTTCCCG ATGACCTGCG CCTTCATAGG TGTTGCCAGC AACTTCACCT TCCTCAGCGT	1200
CATCGTGCTC TTCAGCTACA TGCAGTGGGT GTGGGGGGGC ATCTGGCCCC GACACCGCTT	1260
CTCTTTGCAG GTTAACATCC GAAAAAGAGA CAATTCCCGG AAGGAAGTCC AACGAAGGAT	1320
CTCTGCTCAT CAGCCAGGGC CTGAAGGCCA GGAGGAGTCA ACTCCGCAAT CAGATGTTAC	1380
AGAGGATGGT GAGAGCCCTG AAGATCCCTC AGGGACAGAG GGTCAGCTGT CCGAGGAGGA	1440
GAAACCAGAT CAGCAGCCCC TGAGCGGAGA AGAGGAGCTA GAGCCTGAGG CCAGTGATGG	1500
TTCAGGCTCC TGGGAAGATG CAGCTTTGCT GACGGAGGCC AACCTGCCTG CTCCTGCTCC	1560
TGCTTCTGCT TCTGCCCCTG TCCTAGAGAC TCTGGGCAGC TCTGAACCTG CTGGGGGTGC	1620
TCTCCGACAG CGCCCCACCT GCTCTAGTTC CTGAAGAAAA GGGGCAGACT CCTCACATTC	1680
CAGCACTTTC CCACCTGACT CCTCTCCCCT CGTTTTTCCT TCAATAAACT ATTTTGTGTC	1740
AAAAAAAAAA AAAAA	1755

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Ser Thr Glu Lys Val Asp Gln Lys Glu Glu Ala Gly Glu Lys Glu
 1 5 10 15
 Val Cys Gly Asp Gln Ile Lys Gly Pro Asp Lys Glu Glu Glu Pro Pro
 20 25 30
 Ala Ala Ala Ser His Gly Gln Gly Trp Arg Pro Gly Gly Arg Ala Ala
 35 40 45
 Arg Asn Ala Arg Pro Glu Pro Gly Ala Arg His Pro Ala Leu Pro Ala
 50 55 60
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 65 70 75 80
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
 85 90 95
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu
 100 105 110
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 115 120 125
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 130 135 140
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 145 150 155 160
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 165 170 175
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 180 185 190
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
 195 200 205
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 210 215 220
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 225 230 235 240
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
 245 250 255
 Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
 260 265 270
 Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
 275 280 285
 Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala
 290 295 300

Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	
305					310					315					320	
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	
			325						330					335		
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile	
			340					345					350			
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln	
		355					360					365				
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr	
	370					375					380					
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser	
385					390					395					400	
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp	
				405					410					415		
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro	
			420					425					430			
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro	
		435					440					445				
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser			
	450					455					460					

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGAATAGAGG	ATTTCAAAAA	GCATGCGTTT	TTTGAAGGTC	TAAATTGGGA	AAATATACGA	60
AACCTAGAAG	CACCTTATAT	TCCTGATGTG	AGCAGTCCCT	CTGACACATC	CAACTTCGAC	120
GTGGATGACG	ACGTGCTGAG	AAACACGGAA	ATATTACCTC	CTGGTTCTCA	CACAGGCTTT	180
TCTGGATTAC	ATTTGCCATT	CATTGGTTTT	ACATTCACAA	CGGAAAGCTG	TTTTTCTGAT	240
CGAGGCTCTC	TGAAGAGCAT	AATGCAGTCC	AACACATTAA	CCAAAGATGA	GGATGTGCAG	300
CGGGACCTGG	AGCACAGCCT	GCAGATGGAA	GCTTACGAGA	GGAGGATTCG	GAGGCTGGAA	360
CAGGAGAAGC	TGGAGCTGAG	CAGGAAGCTG	CAAGAGTCCA	CCCAGACCGT	GCAGTCCCTC	420

CACGGCTCAT	CTCGGGCCCT	CAGCAATTCA	AACCGAGATA	AAGAAATCAA	AAAGCTAAAT	480
GAAGAAATCG	AACGCTTGAA	GAATAAAATA	GCAGATTCAA	ACAGGCTGGA	GCGACAGCTT	540
GAGGACACAG	TGGCGCTTCG	CCAAGAGCGT	GAGGACTCCA	CGCAGCGGCT	GCGGGGGCTG	600
GAGAAGCAGC	ACCGCGTGGT	CCGGCAGGAG	AAGGAGGAGC	TGCACAAGCA	ACTGGTTGAA	660
GCCTCAGAGC	GGTTGAAATC	CCAGGCCAAG	GAACTCAAAG	ATGCCCATCA	GCAGCGAAAAG	720
CTGGCCCTGC	AGGAGTTCTC	GGAGCTGAAC	GAGCGCATGG	CAGAGCTCCG	TGCCCAGAAG	780
CAGAAGGTGT	CCCGGCAGCT	GCGAGACAAG	GAGGAGGAGA	TGGAGGTGGC	CACGCAGAAG	840
GTGGACGCCA	TGCGGCAGGA	AATGCGGAGA	GCTGAGAAGC	TCAGGAAAGA	GCTGGAAGCT	900
CAGCTTGATG	ATGCTGTTGC	TGAGGCCTCC	AAGGAGCGCA	AGCTTCGTGA	GCACAGCGAG	960
AACTTCTGCA	AGCAAATGGA	AAGCGAGCTG	GAGGCCCTCA	AGGTGAAGCA	AGGAGGCCGG	1020
GGAGCGGGTG	CCACCTTAGA	GCACCAGCAA	GAGATTTCCA	AAATCAAATC	CGAGCTGGAG	1080
AAGAAAGTCT	TATTTTATGA	AGAGGAATTG	GTCAGACGTG	AGGCCTCCCA	TGTGCTAGAA	1140
GTGAAAAATG	TGAAGAAGGA	GGTGCATGAT	TCAGAAAGCC	ACCAGCTGGC	CCTGCAGAAA	1200
GAAATCTTGA	TGTTAAAAGA	TAAGTTAGAA	AAGTCAAAGC	GAGAACGGCA	TAACGAGATG	1260
GAGGAGGCAG	TAGGTACAAT	AAAAGATAAA	TACGAACGAG	AAAGAGCGAT	GCTGTTTGAT	1320
GAAAACAAGA	AGCTAACTGC	TGAAAATGAA	AAGCTCTGTT	CCTTTGTGGA	TAAACTCACA	1380
GCTCAAAAATA	GACAGCTGGA	GGATGAGCTG	CAGGATCTGG	CAGCCAAGAA	GGAGTCAGTG	1440
GCCCCACTGGG	AAGCTCAGAT	TGCGGAAATC	ATTCAGTGGG	TCAGTGACGA	GAAAGATGCC	1500
CGGGGTTACC	TTCAAGCTCT	TGCTTCCAAG	ATGACCGAAG	AGCTCGAGGC	TTTGAGGAGT	1560
TCTAGTCTGG	GGTCAAGAAC	ACTGGACCCG	CTGTGGAAGG	TGCGCCGCAG	CCAGAAGCTG	1620
GACATGTCCG	CGCGGCTGGA	GCTGCAGTCG	GCCCTGGAGG	CGGAGATCCG	GGCCAAGCAG	1680
CTTGTCCAGG	AGGAGCTCAG	GAAGGTCAAG	GACGCCAACC	TCACCTTGGA	AAGCAAACYA	1740
AWGGATTCCG	AAGCCAAAAA	CAGAGAATTA	TTAGAAGAAA	TGGAATTTT	GAAGAAAAAG	1800
ATGGAAGAAA	AATTCAGAGC	AGATACTGGG	CTCAAACCTC	CAGATTTTCA	GGATTCCATT	1860
TTTGAGTATT	TCAACACTGC	TCCTCTTGCA	CATGACCTGA	CATTTAGAAC	CAGCTCAGCT	1920
AGTGAGCAAG	AAACACAAGC	TCCGAAGCCA	GAAGCGTCCC	CGTCGATGTC	TGTGGCTGCA	1980
TCAGAGCAGC	AGGAGGACAT	GGCTCGGCCC	CCGCAGAGGC	CATCCGCTGT	GCCGTTGCCC	2040
ACCACGCAGG	CCCTGGCTCT	GGCTGGACCG	AAGCCAAAAG	CTCACCAGTT	CAGCATCAAG	2100

TCCTTCTCCA GCCCTACTCA GTGCAGCCAC TGCACCTCCC TGATGGTTGG GCTGATCCGG	2160
CAGGGCTACG CCTGCGAGGT GTGTTTCCTTT GCTTGCCACG TGTCTGCAA AGACGGTGCC	2220
CCCCAGGTGT GCCCAATACC TCCCAGAGCAG TCCAAGAGGC CTCTGGGCGT GGACGTGCAG	2280
CGAGGCATCG GAACAGCCTA CAAAGGCCAT GTCAAGGTCC CAAAGCCCAC GGGGGTGAAG	2340
AAGGGATGGC AGCGCGCATA TGCAGTCGTC TGTGACTGCA AGCTCTTCCT GTATGATCTG	2400
CCTGAAGGAA AATCCACCCA GCCTGGTGTC ATTGCGAGCC AAGTCTTGGA TCTCAGAGAT	2460
GACGAGTTTT CCGTGAGCTC AGTCCTGGCC TCAGATGTCA TTCATGCTAC ACGCCGAGAT	2520
ATTCCATGTA TATTCAGGGT GACGGCCTCT CTCTTAGGTG CACCTTCTAA GACCAGCTCG	2580
CTGCTCATTC TGACAGAAAA TGAGAATGAA AAGAGGAAGT GGGTTGGGAT TCTAGAAGGA	2640
CTCCAGTCCA TCCTTCATAA AAACCGGCTG AGGAATCAGG TCGTGCATGT TCCCTTGGA	2700
GCCTACGACA GCTCGCTGCC TCTCATCAAG GCCATCCTGA CAGCTGCCAT CGTGGATGCA	2760
GACAGGATTG CAGTCGGCCT AGAAGAAGGG CTCTATGTCA TAGAGGTCAC CCGAGATGTG	2820
ATCGTCCGTG CCGCTGACTG TAAGAAGGTA CACCAGATCG AGCTTGCTCC CAGGGAGAAG	2880
ATCGTAATCC TCCTCTGTGG CCGGAACCAC CATGTGCACC TCTATCCGTG GTCGTCCCTT	2940
GATGGAGCGG AAGGCAGCTT TGACATCAAG CTTCCGGAAA CCAAAGGCTG CCAGCTCATG	3000
GCCACGGCCA CACTCAAGAG GARCTCTGGC ACCTGCCTGT TTGTGGCCGT GAAACGGCTG	3060
ATCCTTTGCT ATGAGATCCA GAAAATAAAG CCATATTGAA TGATAAAAAA AAAAAAAAAA	3120
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3180
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	3213

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Met	Gln	Ser	Asn	Thr	Leu	Thr	Lys	Asp	Glu	Asp	Val	Gln	Arg	Asp	Leu
1				5					10					15	
Glu	His	Ser	Leu	Gln	Met	Glu	Ala	Tyr	Glu	Arg	Arg	Ile	Arg	Arg	Leu
			20					25						30	

Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu Ser Thr Gln
 35 40 45
 Thr Val Gln Ser Leu His Gly Ser Ser Arg Ala Leu Ser Asn Ser Asn
 50 55 60
 Arg Asp Lys Glu Ile Lys Lys Leu Asn Glu Glu Ile Glu Arg Leu Lys
 65 70 75 80
 Asn Lys Ile Ala Asp Ser Asn Arg Leu Glu Arg Gln Leu Glu Asp Thr
 85 90 95
 Val Ala Leu Arg Gln Glu Arg Glu Asp Ser Thr Gln Arg Leu Arg Gly
 100 105 110
 Leu Glu Lys Gln His Arg Val Val Arg Gln Glu Lys Glu Glu Leu His
 115 120 125
 Lys Gln Leu Val Glu Ala Ser Glu Arg Leu Lys Ser Gln Ala Lys Glu
 130 135 140
 Leu Lys Asp Ala His Gln Gln Arg Lys Leu Ala Leu Gln Glu Phe Ser
 145 150 155 160
 Glu Leu Asn Glu Arg Met Ala Glu Leu Arg Ala Gln Lys Gln Lys Val
 165 170 175
 Ser Arg Gln Leu Arg Asp Lys Glu Glu Glu Met Glu Val Ala Thr Gln
 180 185 190
 Lys Val Asp Ala Met Arg Gln Glu Met Arg Arg Ala Glu Lys Leu Arg
 195 200 205
 Lys Glu Leu Glu Ala Gln Leu Asp Asp Ala Val Ala Glu Ala Ser Lys
 210 215 220
 Glu Arg Lys Leu Arg Glu His Ser Glu Asn Phe Cys Lys Gln Met Glu
 225 230 235 240
 Ser Glu Leu Glu Ala Leu Lys Val Lys Gln Gly Gly Arg Gly Ala Gly
 245 250 255
 Ala Thr Leu Glu His Gln Gln Glu Ile Ser Lys Ile Lys Ser Glu Leu
 260 265 270
 Glu Lys Lys Val Leu Phe Tyr Glu Glu Glu Leu Val Arg Arg Glu Ala
 275 280 285
 Ser His Val Leu Glu Val Lys Asn Val Lys Lys Glu Val His Asp Ser
 290 295 300
 Glu Ser His Gln Leu Ala Leu Gln Lys Glu Ile Leu Met Leu Lys Asp
 305 310 315 320
 Lys Leu Glu Lys Ser Lys Arg Glu Arg His Asn Glu Met Glu Glu Ala
 325 330 335

Val	Gly	Thr	Ile	Lys	Asp	Lys	Tyr	Glu	Arg	Glu	Arg	Ala	Met	Leu	Phe	340	345	350
Asp	Glu	Asn	Lys	Lys	Leu	Thr	Ala	Glu	Asn	Glu	Lys	Leu	Cys	Ser	Phe	355	360	365
Val	Asp	Lys	Leu	Thr	Ala	Gln	Asn	Arg	Gln	Leu	Glu	Asp	Glu	Leu	Gln	370	375	380
Asp	Leu	Ala	Ala	Lys	Lys	Glu	Ser	Val	Ala	His	Trp	Glu	Ala	Gln	Ile	385	390	395
Ala	Glu	Ile	Ile	Gln	Trp	Val	Ser	Asp	Glu	Lys	Asp	Ala	Arg	Gly	Tyr	405	410	415
Leu	Gln	Ala	Leu	Ala	Ser	Lys	Met	Thr	Glu	Glu	Leu	Glu	Ala	Leu	Arg	420	425	430
Ser	Ser	Ser	Leu	Gly	Ser	Arg	Thr	Leu	Asp	Pro	Leu	Trp	Lys	Val	Arg	435	440	445
Arg	Ser	Gln	Lys	Leu	Asp	Met	Ser	Ala	Arg	Leu	Glu	Leu	Gln	Ser	Ala	450	455	460
Leu	Glu	Ala	Glu	Ile	Arg	Ala	Lys	Gln	Leu	Val	Gln	Glu	Glu	Leu	Arg	465	470	475
Lys	Val	Lys	Asp	Ala	Asn	Leu	Thr	Leu	Glu	Ser	Lys	Xaa	Xaa	Asp	Ser	485	490	495
Glu	Ala	Lys	Asn	Arg	Glu	Leu	Leu	Glu	Glu	Met	Glu	Ile	Leu	Lys	Lys	500	505	510
Lys	Met	Glu	Glu	Lys	Phe	Arg	Ala	Asp	Thr	Gly	Leu	Lys	Leu	Pro	Asp	515	520	525
Phe	Gln	Asp	Ser	Ile	Phe	Glu	Tyr	Phe	Asn	Thr	Ala	Pro	Leu	Ala	His	530	535	540
Asp	Leu	Thr	Phe	Arg	Thr	Ser	Ser	Ala	Ser	Glu	Gln	Glu	Thr	Gln	Ala	545	550	555
Pro	Lys	Pro	Glu	Ala	Ser	Pro	Ser	Met	Ser	Val	Ala	Ala	Ser	Glu	Gln	565	570	575
Gln	Glu	Asp	Met	Ala	Arg	Pro	Pro	Gln	Arg	Pro	Ser	Ala	Val	Pro	Leu	580	585	590
Pro	Thr	Thr	Gln	Ala	Leu	Ala	Leu	Ala	Gly	Pro	Lys	Pro	Lys	Ala	His	595	600	605
Gln	Phe	Ser	Ile	Lys	Ser	Phe	Ser	Ser	Pro	Thr	Gln	Cys	Ser	His	Cys	610	615	620
Thr	Ser	Leu	Met	Val	Gly	Leu	Ile	Arg	Gln	Gly	Tyr	Ala	Cys	Glu	Val	625	630	635
																		640

Cys	Ser	Phe	Ala	Cys	His	Val	Ser	Cys	Lys	Asp	Gly	Ala	Pro	Gln	Val	645	650	655
Cys	Pro	Ile	Pro	Pro	Glu	Gln	Ser	Lys	Arg	Pro	Leu	Gly	Val	Asp	Val	660	665	670
Gln	Arg	Gly	Ile	Gly	Thr	Ala	Tyr	Lys	Gly	His	Val	Lys	Val	Pro	Lys	675	680	685
Pro	Thr	Gly	Val	Lys	Lys	Gly	Trp	Gln	Arg	Ala	Tyr	Ala	Val	Val	Cys	690	695	700
Asp	Cys	Lys	Leu	Phe	Leu	Tyr	Asp	Leu	Pro	Glu	Gly	Lys	Ser	Thr	Gln	705	710	715
Pro	Gly	Val	Ile	Ala	Ser	Gln	Val	Leu	Asp	Leu	Arg	Asp	Asp	Glu	Phe	725	730	735
Ser	Val	Ser	Ser	Val	Leu	Ala	Ser	Asp	Val	Ile	His	Ala	Thr	Arg	Arg	740	745	750
Asp	Ile	Pro	Cys	Ile	Phe	Arg	Val	Thr	Ala	Ser	Leu	Leu	Gly	Ala	Pro	755	760	765
Ser	Lys	Thr	Ser	Ser	Leu	Leu	Ile	Leu	Thr	Glu	Asn	Glu	Asn	Glu	Lys	770	775	780
Arg	Lys	Trp	Val	Gly	Ile	Leu	Glu	Gly	Leu	Gln	Ser	Ile	Leu	His	Lys	785	790	795
Asn	Arg	Leu	Arg	Asn	Gln	Val	Val	His	Val	Pro	Leu	Glu	Ala	Tyr	Asp	805	810	815
Ser	Ser	Leu	Pro	Leu	Ile	Lys	Ala	Ile	Leu	Thr	Ala	Ala	Ile	Val	Asp	820	825	830
Ala	Asp	Arg	Ile	Ala	Val	Gly	Leu	Glu	Glu	Gly	Leu	Tyr	Val	Ile	Glu	835	840	845
Val	Thr	Arg	Asp	Val	Ile	Val	Arg	Ala	Ala	Asp	Cys	Lys	Lys	Val	His	850	855	860
Gln	Ile	Glu	Leu	Ala	Pro	Arg	Glu	Lys	Ile	Val	Ile	Leu	Leu	Cys	Gly	865	870	875
Arg	Asn	His	His	Val	His	Leu	Tyr	Pro	Trp	Ser	Ser	Leu	Asp	Gly	Ala	885	890	895
Glu	Gly	Ser	Phe	Asp	Ile	Lys	Leu	Pro	Glu	Thr	Lys	Gly	Cys	Gln	Leu	900	905	910
Met	Ala	Thr	Ala	Thr	Leu	Lys	Arg	Xaa	Ser	Gly	Thr	Cys	Leu	Phe	Val	915	920	925
Ala	Val	Lys	Arg	Leu	Ile	Leu	Cys	Tyr	Glu	Ile	Gln	Lys	Ile	Lys	Pro	930	935	940

Tyr
945

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGGGCACTT AATCCCAATG AACTGTATGC TTAAAAATAA TTAAATGAT AAAC TTTGTG	60
TTATGTATAC TTTACCACAA TAAGAAAAAG TATTTTAGTA CTAGTGGTAA ATAGTTT TTA	120
TTTAATAGAC TTATATTTTA AAGCTTAAAA ATAATTTAGC TTCTAGAGTA TTACGTT TTT	180
CTTCATGGGA ACTTCAAAAA GCAAGTCACT AAATCCAAGA ATTTTAAAGA AAAAACC CAA	240
ATACATGATT TATGCTGCAT CTGGTATAGA TTTTAAAAAG ACTAGTCAAT CTAAGCTCTA	300
AACTATTAAA TGACAAACCA TTTCATATGT CATTGCATAT TCCTATGTAC CACATTCTCA	360
TATTTCTGTT ATGGGCATGA AGGGGTGTTT GATGCTTCCA TGCCATAATA ACCATGACTA	420
TCACAACCAT TGAAATAAAG GTTCTTGCAG TATTTTCAGG ATGGTCCCAG AAATTTAAAT	480
TAATCTCTCA TCCATTGGCT TTTGCTACTT TAGGTTAATA TTAAATATA ACATACATTT	540
TTGGGGTTTA TGCTGTTAGC TCCAAACCAA AAGATTTTGG AAATTTATTT TGGAAATTTT	600
GTGTTTAGAA TATGAATAAA TCTGCTTATT CAGAAAAATT AAACCTTGAT AACTTGGGAC	660
CTCCTATTCC TGTATGTTCT CTGACATACA TTGAGGGATT TGGCTCTCTT TTGTTTATTT	720
GTTTTACTAG TCAGACATTC CTTTGGCTGC CCATACTTAA TTCTGTTGGG TGTTTCCGCC	780
CCCGCCCTCA GCTTCTGCAG CTACTCTGAT CAACATCCGC AATGCCAGGA AACACTTTGA	840
AAAGCTGGAA AGAGTGGATG GACCAAAGCA GTGTCTTCTC ATGCGCTAAA CATTGATGAA	900
TATTGTTTCA CACAAAAATT AAAAGTTTCC TAATTAATGT TGTATTCATA TATGTAGGCT	960
CTGAAATGTT GTGATGCTTA TTGCTTCTGT ATTTCTTCTC TACTCCCTAG TCTTAATGTT	1020
TAACCTTGAA TGCTATTAAC TTAAATAGCC ATTGAGGAGT TAGAAGATGA ATTGTTTCATG	1080
AAGTCGGTGT TACATAAAAG TAGGTGATAT GTAAGTTTTT TGATAACAAG GTTCTAATAG	1140
TGTTTAAATG TACTGGTAAC CTGGTTCCAA TAGTTGTGTT TGCCCAAGCC TTTCTCGGCA	1200
TCATCTTGTA TTCCTTATCA GATAGTAAGT AACCTGTAAAG TTTGGAGTAT TACTGTTTTT	1260
TCAGCATGCA TTAAAAATAT TCCTTAACTT CAATTGTAAA AAAAAAAAAA AAAAA	1315

[REDACTED]

(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu
65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TAGGCCATGA	AGGCCGAATC	GGCCTTCATG	GCCTACGCTT	ACACAATACC	CACCATGTCC	60
CAGGCTGGTG	CTCAGGAAGC	CCCTATCAAG	AAGAAGCGCC	CCCCTGTGAA	GGAGGAGGAC	120
CTGAAGGGGG	CCCGAGGAAA	CCTGACCAAG	AACCAGGAAA	TCAAGTCCAA	GACCTACCAG	180
GTCATGCGAG	AGTGTGAGCA	AGCTGGCTCG	GCCGCCCGT	CGGTGTTTCT	CCGCACCCGC	240
ACAGGTACCG	AGACTGTCTT	TGAGAAGCCC	AAAGCCGGAC	CCACCAAGAG	TGTCTTCGGC	300
TGAGAAGTGT	GCGCCACTCC	CCTTGCTGCC	CGAATGCTCG	GAAACAGGAG	CCTTACCCAG	360
GAACTCTTTT	TTATGCCAGA	ACGCTTCCTC	TCCCCTGCTG	TCTCTGGGGC	TGCCACCCTC	420

CCCCACAGTC CAGGCCCTTC AGCCAAGGGC TCTGCACCAG CACCTTGGA GCACCAATAA 480
AGAGGATGCC CACGTGGCCC CAGCAAAAAA AAAAAAAAAA 519

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met Lys Ala Glu Ser Ala Phe Met Ala Tyr Ala Tyr Thr Ile Pro Thr
 1 5 10 15
 Met Ser Gln Ala Gly Ala Gln Glu Ala Pro Ile Lys Lys Lys Arg Pro
 20 25 30
 Pro Val Lys Glu Glu Asp Leu Lys Gly Ala Arg Gly Asn Leu Thr Lys
 35 40 45
 Asn Gln Glu Ile Lys Ser Lys Thr Tyr Gln Val Met Arg Glu Cys Glu
 50 55 60
 Gln Ala Gly Ser Ala Ala Pro Ser Val Phe Ser Arg Thr Arg Thr Gly
 65 70 75 80
 Thr Glu Thr Val Phe Glu Lys Pro Lys Ala Gly Pro Thr Lys Ser Val
 85 90 95
 Phe Gly

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GACGGCGACC AAACCCAGCT AGGTCAGACG AGAAAGATAA AACTCTCCA GATGTCTTCC 60
 AGTAATGTCTG AAGTTTTTAT CCCAGTGTCA CAAGGAAACA CCAATGGCTT CCCC GCGACA 120
 GCTTCCAATG ACCTGAAGGC ATTTACTGAA GGAGCTGTGT TAAGTTTTCA TAACATCTGC 180

TATCGAGTAA AACTGAAGAG TGGCTTTCTA CCTTGTCGAA AACCAGTTGA GAAAGAAATA	240
TTATCGAATA TCAATGGGAT CATGAAACCT GGTCTCAACG CCATCCTGGG ACCCACAGGT	300
GGARGCAAAT CTTGTTATT AGATGTCTTA GCTGCAAGGA AAGATCCAAG TGGATTATCT	360
GGAGATGTTT TGATAAATGG AGCACCGCGA CCTGCCAATT TCAAATGTAA TTCAGGTTAC	420
GTGGTACAAG TTGGAACCTCA GTTTATCCGT GGTGTGTCTG GAGGAGAAAAG AAAAAGGACT	480
AGTATAGGAA TGGAGCTTAT CACTGATCCT TCCATCTTGT TCTTGATGA GCCTACAACT	540
GGCTTAGACT CAAGCACAGC AAATGCTGTC CTTTTGCTCC TGAAAAGGAT GTCTAAGCAG	600
GGACGAACAA TCATCTTCTC CATTTCATCAG CCTCGATATT CCATCTTCAA GTTGTTTGAT	660
AGCCTCACCT TATTGGCCTC AGGAAGACTT ATGTTCCACG GGCCTGCTCA GGAGGCCTTG	720
GGATACTTTG AATCAGCTGG TTATCACTGT GAGGCCTATA ATAACCTGC AGACTTCTTC	780
TTGGACATCA TTAATGGAGA TTCCACTGCT GTGGCATTAA ACAGAGAAGA AGACTTTAAA	840
GCCACAGAGA TCATAGAGCC TTCCAAGCAG GATAAGCCAC TCATAGAAAA ATTAGCGGAG	900
ATTTATGTCA ACTCCTCCTT CTACAAAGAG ACAAAGCTG AATTACATCA ACTTTCCGGG	960
GGTGAGAAGA AGAAGAAGAT CACAGTCTTC AAGGAGATCA GCTACACCAC CTCCTTCTGT	1020
CATCAACTCA GATGGGTTTC CAAGCGTTCA TTCAAAAACCT TGCTGGGTAA TCCCAGGCC	1080
TCTATAGCTC AGATCATTTGT CACAGTCGTA CTGGGACTGG TTATAGGTGC CATTTACTTT	1140
GGGCTAAAAA ATGATTCTAC TGGAATCCAG AACAGAGCTG GGGTTCTCTT CTTCTGACG	1200
ACCAACCAGT GTTTCAGCAG TGTTTCAGCC GTGGAACCTCT TTGTGGTAGA GAAGAAGCTC	1260
TTCATACATG AATACATCAG CGGATACTAC AGAGTGTGAT CTTATTTCTT TGGAAAACCTG	1320
TTATCTGATT TATTACCCAT GAGGATGTTA CCAAGTATTA TATTTACCTG TATAGTGATC	1380
TTCATGTTAG GATTGAAGCC AAAGGCAGAT GCCTTCTTCG TTATGATGTT TACCCTTATG	1440
ATGGTGGCTT ATTCAGCCAG TTCCATGGCA CTGGCCATAG CAGCAGGTCA GAGTGTGGTT	1500
TCTGTAGCAA CACTTCTCAT GACCATCTGT TTTGTGTTTA TGATGATTTT TTCAGGTCTG	1560
TTGGTCAATC TCACAACCAT TGCATCTTGG CTGTCATGGC TTCAGTACTT CAGCATTTCA	1620
CGATATGGAT TTACGGCTTT GCAGCATAAT GAATTTTTTG GACAAAACCT CTGCCCAGGA	1680
CTCAATGCAA CAGGAAACAA TCCTTGTAAC TATGCAACAT GTACTGGCGA AGAATATTTG	1740
GTAAAGCAGG GCATCGATCT CTCACCCTGG GGCTTGTGGA AGAATCACGT GGCCTTGGCT	1800
TGTATGATTG TTATTTTCTT CACAATTGCC TACCTGAAAT TGTTATTTCT TAAAAAATAT	1860

TCTTAAATTT CCCCTTAATT CAGTATGATT TATCCTCACA TAAAAAAGAA GCACTTTGAT	1920
TGAAGTATTC AATCAAGTTT TTTTGGTTGT TTTCTGTTCC CTTGCCATCA CACTGTTGCA	1980
CAGCAGCAAT TGTTTTAAAG AGATACATTT TTAGAAATCA CAACAACTG AATTAAACAT	2040
GAAAGAACCC AAGACATCAT GTATCGCATA TTAGTTAATC TCCTCAGACA GTAACCATGG	2100
GGAAGAAATC TGGTCTAATT TATTAATCTA AAAAAGGAGA ATTGAATTCT GGAAACTCCT	2160
GACAAGTTAT TACTGTCTCT GGCATTTGTT TCCTCATCTT TAAAATGAAT AGGTAGGTTA	2220
GTAGCCCTTC AGTCTTAATA CTTTATGATG CTATGGTTTG CCATTATTTA ATAAATGACA	2280
AATGTATTAA TGCTAAAAA AAAAAAAAAA AGCGGCCTTC ATGGCCTAGA GATTTCAACT	2340
TAACCTTGACC GCTCTGAGCT AAACCTAGCC CCAAACCCAC TCCACCTTAT TACCAGACAA	2400
CCTTAACCAA ACCATTTACC CAAATAAAGT ATAGGCGATA GAAATTGAAA CCTGGCGCAA	2460
TAGATATAGT ACCGCAAGGG AAAGATGAAA AATTATAACC AAGCATAATA TAGCAAGGAC	2520
TAACCCCTAT ACCTTCTGCA TAATGAATTA ACTAGAAATA ACTTTGCAAG GAGAGCCAAA	2580
GCTAAGACCC CCGAAACCAG ACGAGCTACC TAAGAACAGC TAAAAGAGCA CACCCGTCTA	2640
TGTAGCAAAA TAGTGGGAAG ATTTATAGGT AGAGGCGACA AACCTACCGA GCCTGGTGAT	2700
AGCTGGTTGT CCCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2760
AAAAAAAAAA AAAAAAAAAA AAAAAAAA	2788

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met	Ser	Ser	Ser	Asn	Val	Glu	Val	Phe	Ile	Pro	Val	Ser	Gln	Gly	Asn
1				5					10					15	
Thr	Asn	Gly	Phe	Pro	Ala	Thr	Ala	Ser	Asn	Asp	Leu	Lys	Ala	Phe	Thr
			20					25					30		
Glu	Gly	Ala	Val	Leu	Ser	Phe	His	Asn	Ile	Cys	Tyr	Arg	Val	Lys	Leu
		35					40					45			
Lys	Ser	Gly	Phe	Leu	Pro	Cys	Arg	Lys	Pro	Val	Glu	Lys	Glu	Ile	Leu
	50					55					60				

Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
 65 70 75 80
 Pro Thr Gly Gly Xaa Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
 85 90 95
 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
 100 105 110
 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Val Gly
 115 120 125
 Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys Arg Thr Ser
 130 135 140
 Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe Leu Asp Glu
 145 150 155 160
 Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val Leu Leu Leu
 165 170 175
 Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe Ser Ile His
 180 185 190
 Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu
 195 200 205
 Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu Ala Leu Gly
 210 215 220
 Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala
 225 230 235 240
 Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala Val Ala Leu
 245 250 255
 Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys
 260 265 270
 Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser
 275 280 285
 Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu Ser Gly Gly
 290 295 300
 Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr
 305 310 315 320
 Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser Phe Lys Asn
 325 330 335
 Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile Val Thr Val
 340 345 350
 Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp
 355 360 365

Ser	Thr	Gly	Ile	Gln	Asn	Arg	Ala	Gly	Val	Leu	Phe	Phe	Leu	Thr	Thr	370	375	380
Asn	Gln	Cys	Phe	Ser	Ser	Val	Ser	Ala	Val	Glu	Leu	Phe	Val	Val	Glu	385	390	395 400
Lys	Lys	Leu	Phe	Ile	His	Glu	Tyr	Ile	Ser	Gly	Tyr	Tyr	Arg	Val	Ser	405	410	415
Ser	Tyr	Phe	Leu	Gly	Lys	Leu	Leu	Ser	Asp	Leu	Leu	Pro	Met	Arg	Met	420	425	430
Leu	Pro	Ser	Ile	Ile	Phe	Thr	Cys	Ile	Val	Tyr	Phe	Met	Leu	Gly	Leu	435	440	445
Lys	Pro	Lys	Ala	Asp	Ala	Phe	Phe	Val	Met	Met	Phe	Thr	Leu	Met	Met	450	455	460
Val	Ala	Tyr	Ser	Ala	Ser	Ser	Met	Ala	Leu	Ala	Ile	Ala	Ala	Gly	Gln	465	470	475 480
Ser	Val	Val	Ser	Val	Ala	Thr	Leu	Leu	Met	Thr	Ile	Cys	Phe	Val	Phe	485	490	495
Met	Met	Ile	Phe	Ser	Gly	Leu	Leu	Val	Asn	Leu	Thr	Thr	Ile	Ala	Ser	500	505	510
Trp	Leu	Ser	Trp	Leu	Gln	Tyr	Phe	Ser	Ile	Pro	Arg	Tyr	Gly	Phe	Thr	515	520	525
Ala	Leu	Gln	His	Asn	Glu	Phe	Leu	Gly	Gln	Asn	Phe	Cys	Pro	Gly	Leu	530	535	540
Asn	Ala	Thr	Gly	Asn	Asn	Pro	Cys	Asn	Tyr	Ala	Thr	Cys	Thr	Gly	Glu	545	550	555 560
Glu	Tyr	Leu	Val	Lys	Gln	Gly	Ile	Asp	Leu	Ser	Pro	Trp	Gly	Leu	Trp	565	570	575
Lys	Asn	His	Val	Ala	Leu	Ala	Cys	Met	Ile	Val	Ile	Phe	Leu	Thr	Ile	580	585	590
Ala	Tyr	Leu	Lys	Leu	Leu	Phe	Leu	Lys	Lys	Tyr	Ser					595	600	

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CGACTTCCTC	GGCTGCGCGG	CGCTCGCGCG	GAGCTCCCCG	GCCGGCGGTG	CGTCCCCACG	60
GTCACCATGA	AAGACGACTT	CGCAGAGGAG	GAGGAGGTGC	AATCCTTCGG	TTACAAGCGG	120
TTTGGTATTC	AGGAAGGAAC	ACAATGTACC	AAATGTAAAA	ATAACTGGGC	ACTGAAGTTT	180
TCTATCATAT	TATTATACAT	TTTGTGTGCC	TTGCTAACAA	TCACAGTAGC	CATTTTGGGA	240
TATAAAGTTG	TAGAGAAAAAT	GGACAATGTC	ACAGGTGGCA	TGGAAACATC	TCGCCAAACC	300
TATGATGACA	AGCTCACAGC	AGTGGAAGT	GACCTGAAAA	AATTAGGTGA	CCAAACTGGG	360
AAGAAAGCTA	TCAGCACCAA	CTCAGAACTC	TCCACCTTCA	GATCAGACAT	TCTAGATCTC	420
CGTCAGCAAC	TTCGTGAGAT	TACAGAAAAA	ACCAGCAAGA	ACAAGGATAC	GCTGGAGAAG	480
TTACAGGCGA	GCGGGGATGC	TCTGGTGGAC	AGGCAGAGTC	AATTGAAAGA	AACTTTGGAG	540
AATAACTCTT	TCCTCATCAC	CACTGTAAAC	AAAACCCCTC	AGGCGTATAA	TGGCTATGTC	600
ACGAATCTGC	AGCAAGATAC	CAGCGTGCTC	CAGGGCAATC	TGCAGAACCA	AATGTATTCT	660
CATAATGTGG	TCATCATGAA	CTCAACAACC	TGAACCTGAC	CCAGGTGCAG	CAGAGGAACC	720
TCATCACGAA	TCTGCAGCGG	TCTGTGGATG	ACACAAGCCA	GGCTATCCAG	CGAATCAAGA	780
ACGACTTTCA	AAATCTGCAG	CAGGTTTTTC	TTCAAGCCAA	GAAGGACACG	GATTGGCTGA	840
AGGAGAAAGT	GCAGAGCTTG	CAGACGCTGG	CTGCCAACAA	CTCTGCGTTG	GCCAAAGCCA	900
ACAACGACAC	CCTGGAGGAT	ATGAACAGCC	AGCTCAACTC	ATTCACAGGT	CAGATGGAGA	960
ACATCACCAC	TATCTCTCAA	GCCAACGAGC	AGAACCTGAA	AGACCTGCAG	GACTTACACA	1020
AAGATGCAGA	GAATAGAACA	GCCATCAAGT	TCAACCAACT	GGAGGAACGC	TTCCAGCTCT	1080
TTGAGACGGA	TATTGTGAAC	ATCATTAGCA	ATATCAGTTA	CACAGCCCAC	CACCTGCGGA	1140
CGCTGACCAG	CAATCTAAAT	GAAGTCAGGA	CCACTTGCAC	AGATACCCTT	ACCAAACACA	1200
CAGATGATCT	GACCTCCTTG	AATAATACCC	TGGCCAACAT	CCGTTTGGAT	TCTGTTTCTC	1260
TCAGGATGCA	ACAAGATTTG	ATGAGGTCGA	GGTTAGACAC	TGAAGTAGCC	AACTTATCAG	1320
TGATTATGGA	AGAAATGAAG	CTAGTAGACT	CCAAGCATGG	TCAGCTCATC	AAGAATTTTA	1380
CAATACTACA	AGGTCCACCG	GGCCCCAGGG	GTCCAAGAGG	TGACAGAGGA	TCCCAGGGAC	1440
CCCCTGGCCC	AACTGGCAAC	AAGGGACAGA	AAGGAGAGAA	GGGGGAGCCT	GGACCACCTG	1500
GCCCTGCGGG	TGAGAGAGGC	CCAATTGGAC	CAGCTGGTCC	CCCCGGAGAG	CGTGGCGGCA	1560
AAGGATCTAA	AGGCTCCCAG	GGCCCCAAAG	GCTCCCGTGG	TTCCCCTGGG	AAGCCCGGCC	1620
CTCAGGGCCC	CAGTGGGGAC	CCAGGCCCCC	CGGGCCCACC	AGGCAAAGAG	GGACTCCCCG	1680

GCCCTCAGGG CCCTCCTGGC TTCCAGGGAC TTCAGGGCAC CGTTGGGGAG CCTGGGGTGC	1740
CTGGACCTCG GGGACTGCCA GGCTTGCCTG GGGTACCAGG CATGCCAGGC CCCAAGGGCC	1800
CCCCGGGCCC TCCTGGCCCA TCAGGAGCGG TGGTGGCCCT GGCCCTGCAG AATGAGCCAA	1860
CCCCGGCACC GGAGGACAAT AGCTGCCCCG CTCACTGGAA GAACTTCACA GACAAATGCT	1920
ACTATTTTTC AGTTGAGAAA GAAATTTTTC AGGATGCAAA GCTTTTCTGT GAAGACAAGT	1980
CTTCACATCT TGTTCATATA AACACTAGAG AGGAACAGCA ATGGATAAAA AAACAGATGG	2040
TAGGGAGAGA GAGCCACTGG ATCGGCCTCA CAGACTCAGA GCGTGAAAAT GAATGGAAGT	2100
GGCTGGATGG GACATCTCCA GACTACAAAA ATTGGAAAGC TGGACAGCCG GATAACTGGG	2160
GTCATGGCCA TGGGCCAGGA GAAGACTGTG CTGGGTTGAT TTATGCTGGG CAGTGGAACG	2220
ATTTCCAATG TGAAGACGTC AATAACTTCA TTTGCGAAAA AGACAGGGAG ACAGTACTGT	2280
CATCTGCATT ATAACGGACT GTGATGGGAT CACATGAGCA AATTTTCAGC TCTCAAAGGC	2340
AAAGGACACT CCTTTCTAAT TGCATCACCT TCTCATCAGA TTGAAAAAAA AAAAGCACTG	2400
AAAGCCAATT ACTGAAAAA AATTGACAGC TAGTGTTTTT TACCATCCGT CATTACCCAA	2460
AGACTTGGGA ACTAAAATGT TCCCCAGGGT GATATGCTGA TTTTCATTGT GCACATGGAC	2520
TGAATCACAT AGATTCTCCT CCGTCAGTAA CCGTGCGATT ATACAAATTA TGTCTTCCAA	2580
AGTATGGAAC ACTCCAATCA GAAAAAGGTT ATCATTGGTC GTTGAGTTAT GGGAAGAACT	2640
TAAGCATATA CTGTGTAAAC AGTGCCATAC ATTTCTAAAA TCCCAAGTGT AGGAAAAATA	2700
TGCAGACATA CAGATATATA GGCCAACTAT TAGTAATAAT ATGAAATATA CTTAAAGAGC	2760
TTTTAAAACT TTGTATTTTT GTACAAAATA TTTGTCTTTT ACAATTTTTT TCCTTTTTTT	2820
TTTTTTGTCA TTTTACCGAC ATAATACATG GAGCCAAAGA AAACAATAAT GGTACTAATA	2880
AAAACCTCTA GGGTTTCCTG TCAGATTTAA TTCTAAAAA AAAAAAAAAA	2930

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Lys Asp Asp Phe Ala Glu Glu Glu Glu Val Gln Ser Phe Gly Tyr

1	5	10	15
Lys Arg Phe Gly Ile Gln Glu Gly Thr Gln Cys Thr Lys Cys Lys Asn	20	25	30
Asn Trp Ala Leu Lys Phe Ser Ile Ile Leu Leu Tyr Ile Leu Cys Ala	35	40	45
Leu Leu Thr Ile Thr Val Ala Ile Leu Gly Tyr Lys Val Val Glu Lys	50	55	60
Met Asp Asn Val Thr Gly Gly Met Glu Thr Ser Arg Gln Thr Tyr Asp	65	70	75
Asp Lys Leu Thr Ala Val Glu Ser Asp Leu Lys Lys Leu Gly Asp Gln	85	90	95
Thr Gly Lys Lys Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg	100	105	110
Ser Asp Ile Leu Asp Leu Arg Gln Gln Leu Arg Glu Ile Thr Glu Lys	115	120	125
Thr Ser Lys Asn Lys Asp Thr Leu Glu Lys Leu Gln Ala Ser Gly Asp	130	135	140
Ala Leu Val Asp Arg Gln Ser Gln Leu Lys Glu Thr Leu Glu Asn Asn	145	150	155
Ser Phe Leu Ile Thr Thr Val Asn Lys Thr Leu Gln Ala Tyr Asn Gly	165	170	175
Tyr Val Thr Asn Leu Gln Gln Asp Thr Ser Val Leu Gln Gly Asn Leu	180	185	190
Gln Asn Gln Met Tyr Ser His Asn Val Val Ile Met Asn Ser Thr Thr	195	200	205

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCTATATATT TTTTCTAGGA AGGGGTGTTT TTCTTTCTGA TTTAATTCCC TACATTTTTC	60
TCTTTCATAT GAAGTTGCAG ATAATGTTTT TCCTTCGGAT TTTTATTCTT TAAGATTTTT	120
AACCTGTGCA AGACTTTTTC AATGATACAA GTCAAGGAGG ATGAAGATCT TTTTCCACTT	180

CAGTCTTCAC	TTTGCTCCAG	CTATTGCTAA	GAAAGGCACA	AACAATGACA	GCATATTTAA	240
GGAAGAACCT	GGCCGGCTTG	GGTCACCGCT	GCTGTCTTTC	TTGGTTTTGC	GTCTACCTGG	300
GAGAGCCCAG	CTTTTAGGTT	CCCATTGAGG	GAAGCATGAG	AGAGGATTGT	TTGGGGGATG	360
CTGCCAGAGC	TTCCAGCTGA	CAGTCTCTGC	AGAGCGGCTG	CCAAGTGGCC	TGGTGGCCGT	420
ATGTTGGCAG	TTTTTGATGA	ATTGGGATTA	GGGAATGTTT	GTTTACTTGA	TAACCGAGTG	480
TCTACAAGGA	GAGGTGGCAG	CGTGAGGGAA	TAGTGCCACC	ATAATGAGGA	CACAGCCAGC	540
CATCTCTTCC	CTGCCACAGA	ACCCAGGCA	GTCCCCTTCA	GGCTACAGTT	TTCCATCTGG	600
ACCGAGGGAC	TGGCCGGTGC	AGCAGGAGGA	GCCGATCACC	CTCTGTGGGA	ACGAGGATGC	660
CCAGAAGTTC	CAGTTACTGT	GGCTCCATGG	TCCCCTTCTC	GATGCGCATC	TTGCACGCGG	720
AGCTTCAGCA	GTACCTGGGG	AACCCACAGG	AGTCGCTGGA	TAGACTGCAC	AAGGTGAAGA	780
CTGTCTGCAG	CAAGATCCTG	GCCAATTTGG	AGCAAGGCTT	AGCAGAAGAC	GGCGGCATGA	840
GCAGCGTGAC	TCAGGAGGGC	AGACAAGCCT	CTATCCGGCT	GTGGAGGTCA	CGTCTGGGCC	900
GGGTGATGTA	CTCCATGGCA	AACTGTCTGC	TCCTGATGAA	GGATTATGTG	CTGGCCGTGG	960
AGGCGTATCA	TTCGGTTATC	AAGTATTACC	CAGAGCAAGA	GCCCCAGCTG	CTCAGCGGCA	1020
TCGGCCGGAT	TTCCCTGCAG	ATTGGAGACA	TAAAAACAGC	TGAAAAGTAT	TTCAAGACG	1080
TTGAGAAAGT	AACACAGAAA	TTAGATGGAC	TACAGGGTAA	AATCATGGTT	TTGATGAACA	1140
GCGCGTTTCT	TCACCTCGGG	CAGAATAACT	TTGCAGAAGC	CCACAGGTTC	TTACAGAGA	1200
TCTTAAGGAT	GGATCCAAGA	AACGCAGTGG	CCAACAACAA	CGCTGCCGTG	TGTCTGCTCT	1260
ACCTGGGCAA	GCTCAAGGAC	TCCCTGCGGC	AGCTGGAGGC	CATGGTCCAG	CAGGACCCCA	1320
GGCACTACCT	GCACGAGAGC	GTGCTCTTCA	ACCTGACCAC	CATGTACGAG	CTGGAGTCCT	1380
CACGGAGCAT	GCAGAAGAAA	CAGGCCCTGC	TGGAGGCTGT	CGCCGGCAAG	GAGGGGGACA	1440
GCTTCAACAC	ACAGTGCCTC	AAGCTGGCCT	AGCTGCCTCC	AACACACTAC	GTCAGAAGGA	1500
CCCGGTCTT	TGAAACTGTG	TCTTGAAGCT	AATGTATTAA	TGTGACATGG	AGGAACTCAA	1560
TAAAACTCCT	GCTTCAAAAA	AAAAAAAAAA				1589

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Met	Pro	Arg	Ser	Ser	Ser	Tyr	Cys	Gly	Ser	Met	Val	Pro	Phe	Ser	Met	
1				5					10					15		
Arg	Ile	Leu	His	Ala	Glu	Leu	Gln	Gln	Tyr	Leu	Gly	Asn	Pro	Gln	Glu	
			20				25						30			
Ser	Leu	Asp	Arg	Leu	His	Lys	Val	Lys	Thr	Val	Cys	Ser	Lys	Ile	Leu	
		35				40						45				
Ala	Asn	Leu	Glu	Gln	Gly	Leu	Ala	Glu	Asp	Gly	Gly	Met	Ser	Ser	Val	
	50					55					60					
Thr	Gln	Glu	Gly	Arg	Gln	Ala	Ser	Ile	Arg	Leu	Trp	Arg	Ser	Arg	Leu	
65					70					75					80	
Gly	Arg	Val	Met	Tyr	Ser	Met	Ala	Asn	Cys	Leu	Leu	Leu	Met	Lys	Asp	
				85					90					95		
Tyr	Val	Leu	Ala	Val	Glu	Ala	Tyr	His	Ser	Val	Ile	Lys	Tyr	Tyr	Pro	
			100					105					110			
Glu	Gln	Glu	Pro	Gln	Leu	Leu	Ser	Gly	Ile	Gly	Arg	Ile	Ser	Leu	Gln	
		115					120					125				
Ile	Gly	Asp	Ile	Lys	Thr	Ala	Glu	Lys	Tyr	Phe	Gln	Asp	Val	Glu	Lys	
	130					135					140					
Val	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Gln	Gly	Lys	Ile	Met	Val	Leu	Met	
145				150						155					160	
Asn	Ser	Ala	Phe	Leu	His	Leu	Gly	Gln	Asn	Asn	Phe	Ala	Glu	Ala	His	
			165						170					175		
Arg	Phe	Phe	Thr	Glu	Ile	Leu	Arg	Met	Asp	Pro	Arg	Asn	Ala	Val	Ala	
			180					185					190			
Asn	Asn	Asn	Ala	Ala	Val	Cys	Leu	Leu	Tyr	Leu	Gly	Lys	Leu	Lys	Asp	
		195					200					205				
Ser	Leu	Arg	Gln	Leu	Glu	Ala	Met	Val	Gln	Gln	Asp	Pro	Arg	His	Tyr	
	210					215					220					
Leu	His	Glu	Ser	Val	Leu	Phe	Asn	Leu	Thr	Thr	Met	Tyr	Glu	Leu	Glu	
225				230						235					240	
Ser	Ser	Arg	Ser	Met	Gln	Lys	Lys	Gln	Ala	Leu	Leu	Glu	Ala	Val	Ala	
			245					250						255		
Gly	Lys	Glu	Gly	Asp	Ser	Phe	Asn	Thr	Gln	Cys	Leu	Lys	Leu	Ala		
		260					265						270			

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TATAAAGAGT GACTCTCCTA TGAAGGTAAA GGCCACCCCT CTTCAGTTCC AGTGACTGAG 60
ATACATTTTT CCAATCCTGG GGGCAAATAC AGACACAGCA AGTTCCTTCT TCCCTTTGGA 120
AATTTGGCAG CTGCCTTCAC CAGTGAGCAC AAAGCCACAT TTCAAAGGAA ACTGACAAAT 180
TATCCCCAGC TGCCAGAAGA AGAAATCCTC ACTGGACGGC TTCCTGTTTC CTGTGGTTCA 240
TTATCTGATT GGCTGCAGGG ATGAAAGTTT TTAAGTTCAT AGGACTGATG ATCCTCCTCA 300
CCTCTGCGTT TTCAGCCGGT TCAGGACAAA GTCCAATGAC TGTGCTGTGC TCCATAGACT 360
GGTTCATGGT CACAGTGCAC CCCTTCATGC TAAACAACGA TGTGTGTGTA CACTTTCATG 420
AACTACACTT GGGCCTGGGT TGCCCCCCAA ACCATGTTCA GCCACACGCC TACCAGTTCA 480
CCTACCGTGT TACTGAATGT GGCATCAGGG CCAAAGCTGT CTCTCAGGAC ATGGTTATCT 540
ACAGCACTGA GATACACTAC TCTTCTAAGG GCACGCCATC TAAGTTTGTG ATCCCAGTGT 600
CATGTGCTGC CCCCCAAAAG TCCCCATGGC TCACCAAGCC CTGCTCCATG AGAGTAGCCA 660
GCAAGAGCAG GGCCACAGCC CAGAAGGATG AGAAATGCTA CGAGGTGTTT AGCTTGTCAC 720
AGTCCAGTCA AAGGCCCAAC TGCGATTGTC CACCTTGTGT CTTCAGTGAA GAAGAGCATA 780
CCCAGGTCCC TTGTCACCAA GCAGGGGCTC AGGAGGCTCA ACCTCTGCAG CCATCTCACT 840
TTCTTGATAT TTCTGAGGAT TGGTCTCTTC ACACAGATGA TATGATTGGG TCCATGTGAT 900
CCTCAGGTTT GGGGTCTCCT GAAGATGCTA TTTCTAGAAT TAGTATATAG TGTACAAATG 960
TCTGACAAAT AAGTGCTCTT GTGACCCCTCA TGTGAGCACT TTTGAGAAAG AGAAACCTAT 1020
AGCAACTTCA TGAATTAAGC CTTTTTCTAT ATTTTATAT TCATGTGTAA ACAAAAAATA 1080
AAATAAAATT CTGATCGCAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
AAAAAAAAAA AAA 1153

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Met	Lys	Val	Phe	Lys	Phe	Ile	Gly	Leu	Met	Ile	Leu	Leu	Thr	Ser	Ala	
1				5					10					15		
Phe	Ser	Ala	Gly	Ser	Gly	Gln	Ser	Pro	Met	Thr	Val	Leu	Cys	Ser	Ile	
			20					25					30			
Asp	Trp	Phe	Met	Val	Thr	Val	His	Pro	Phe	Met	Leu	Asn	Asn	Asp	Val	
			35				40					45				
Cys	Val	His	Phe	His	Glu	Leu	His	Leu	Gly	Leu	Gly	Cys	Pro	Pro	Asn	
	50					55					60					
His	Val	Gln	Pro	His	Ala	Tyr	Gln	Phe	Thr	Tyr	Arg	Val	Thr	Glu	Cys	
	65				70					75					80	
Gly	Ile	Arg	Ala	Lys	Ala	Val	Ser	Gln	Asp	Met	Val	Ile	Tyr	Ser	Thr	
				85					90					95		
Glu	Ile	His	Tyr	Ser	Ser	Lys	Gly	Thr	Pro	Ser	Lys	Phe	Val	Ile	Pro	
			100					105					110			
Val	Ser	Cys	Ala	Ala	Pro	Gln	Lys	Ser	Pro	Trp	Leu	Thr	Lys	Pro	Cys	
		115					120						125			
Ser	Met	Arg	Val	Ala	Ser	Lys	Ser	Arg	Ala	Thr	Ala	Gln	Lys	Asp	Glu	
	130					135						140				
Lys	Cys	Tyr	Glu	Val	Phe	Ser	Leu	Ser	Gln	Ser	Ser	Gln	Arg	Pro	Asn	
	145				150				155						160	
Cys	Asp	Cys	Pro	Pro	Cys	Val	Phe	Ser	Glu	Glu	Glu	His	Thr	Gln	Val	
			165						170					175		
Pro	Cys	His	Gln	Ala	Gly	Ala	Gln	Glu	Ala	Gln	Pro	Leu	Gln	Pro	Ser	
			180					185					190			
His	Phe	Leu	Asp	Ile	Ser	Glu	Asp	Trp	Ser	Leu	His	Thr	Asp	Asp	Met	
		195					200						205			
Ile	Gly	Ser	Met													
			210													

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4285 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTAATCTGT	GTCTCCAGCA	TTTATTTTTT	TGTTTGTGTC	ATCGGGTTCC	TGGTTTTCTT	60
TTAAGACATA	GTCAACTGTG	TGGACCTGTA	GGTTTGGGGC	AGCAACCAAT	TCCATTGTTT	120
TCCTTTTTGT	CAAATCCAAG	AGAAAATATA	CCATAAGGAG	CTAGAAGATT	CTAGTTCACA	180
GCCTTTTGAA	TCTTCATGGC	CTTTGAATCC	TCATGGCCTC	TGAAATCTGA	ATCAGTTTTC	240
TCCCAGGARG	TCTCTGGGGG	CTGAGCTGCT	ACAGGGGCAR	ARGGTGGGGT	GGGGTTGGGT	300
GGGARAATCA	TCCTGGCACT	TCATCGTGCA	TGCTATTTTCG	GGCAGCATCT	TTTTTTTTTT	360
ATTTTATTAT	TATTTTTTTT	CCTGATGCTT	GAGTTATGAA	TGAGGATGAC	CTCTGCAATC	420
ATGATGTCTC	CCATAGACTC	TGTTCCCTTG	TCCTTTGCCA	GCTTTCTCAT	GCATGGTCCT	480
AACACTTCCA	TGATTTAATC	TGCTGCAGGA	CCATAGTCTT	CAGCCACCTC	AGCAATAACT	540
TGTTAGAACA	TTAAAAGGAA	GTAAATTGAG	AACAACTTGT	TGCCATCCCA	TTTTCATTAG	600
AAATCAGACA	TCTTAGAGAT	GTCAAGAAAG	CAGCTAGCAG	CTAGGGGGTA	TGGGGACCTG	660
TCCTGCTCAC	ACTGCTGTGT	GTCAGACCAG	ACCTGATCCT	GGAGCTCAGG	ACCCTAGAGA	720
GCCCTGATCT	CTGGAACTCT	TGCCACGTTG	TTGCTGAGGC	AGCTGAAGTC	CCCATCTCCC	780
ACCATAACAA	TCACAAATAG	ACAGTAGTGG	AGCCAGCATC	CCCAGGCCCC	TTTTTGTGTA	840
AGCAGAAAGG	GAGCTGTGAG	CCTTGCCCTG	TTTGCAGGTG	TCAAGTGCCT	CTCCCTGCCT	900
GTACTTCTCC	CCTTCCTCTG	AGCAGAGCTT	TGGTAGCTGT	TGCCAATGCA	AAGAAATGTA	960
AAGCAGCAAA	AGAAGACAGC	AGGTTCTGAC	CTGAGGAGGG	AAACCAAATT	TATCCCACAA	1020
AGGCCCATTA	ACCCACCCCC	CCTCGCCTCC	CACCCCCAGA	CTGGATCCAC	TACTGGCCCCA	1080
AGAATACTGA	TGAGAAACCT	AGTCTGGATT	GGGTCGGAAG	CTGGAATTTG	GTGCTCTGCA	1140
GACCAGTGCT	CAAAATTGTG	GTTATTTTTT	AGGACTCGCC	TTCAATCCAG	AACATTTGCG	1200
TTTCACCTTC	CTCGCCCA	TCCAGTTAAC	AAGGTAGCTC	ATCACTTCTT	GCATCTGTTG	1260
AGTGACATGC	TGGATTTTAA	TTTTTATTGT	GGTTGTACTT	GGATGCAAGG	AATATGTTTT	1320
GTTCTCCCA	ATTTAGCGCA	CCATCCTGGG	AAGTGCATGT	CTCAGACCAA	CTCCACCTTC	1380
ACCTTCACCA	CCTGTCGCAT	CCTGCATCCT	TCAGATGAGC	TCACTCGGGT	CACACCAAGC	1440
CTTAACCTCAG	CCCCAACTCC	AGCTTGTGGC	AGCACCAGCC	ACTTGAAATC	CACGCCGGTG	1500

GCCACACCAT	GCACTCCACG	GAGACTGAGC	CTGGCTGAGT	CCTTCACTAA	CACCCGTGAG	1560
TCCACGACCA	CCATGAGCAC	ATCCCTGGGG	CTCGTGTGGC	TGTTGAAGGA	GCGGGGCATT	1620
TCTGCTGCCG	TGTACGACCC	CCAGAGCTGG	GACAGGGCCG	GCCGGGGCTC	CCTCCTGCAC	1680
TCCTACACGC	CCAAGATGGC	TGTGATCCCC	TCTACTCCGC	CGAACTCGCC	TATGCAGACA	1740
CCCACATCCT	CCCCACCCTC	CTTTGAGTTC	AAGTGCACGA	GCCCTCCCTA	CGACAATTTT	1800
CTGGCTTCCA	AGCCAGCCAG	CTCCATCCTG	AGGGAAGTGA	GAGAAAAGAA	CGTCCGCAGC	1860
AGCGAGAGCC	AGACCGACGT	GTCCGTCTCC	AACCTCAACC	TCGTGGACAA	AGTCAGGAGG	1920
TTTGGGGTGG	CCAAAGTGGT	GAACTCAGGG	CGAGCCCATG	TCCCCACCTT	GACTGAGGAG	1980
CAGGGACCCC	TCCTCTGTGG	GCCCCCGGGG	CCAGCACCAG	CCCTTGTTCC	CAGAGGCCTG	2040
GTACCTGAGG	GCCTGCCCCT	CAGATGCCCC	ACTGTCACCA	GTGCCATCGG	TGGGCTGCAG	2100
CTCAATAGTG	GCATCCGGCG	GAATCGCAGC	TTCCCCACCA	TGGTGGGATC	TAGCATGCAG	2160
ATGAAAGCTC	CTGTGACTCT	CACCTCGGGC	ATCTTGATGG	GTGCTAAGCT	CTCCAAACAA	2220
ACTAGCTTAC	GGTGAGGACT	GGAGGGGGGC	CGGTTGCCCT	AGAGGAGACC	CACGTTCTCT	2280
CTTGCTCCCA	CCTCCCTCTC	TTCCCCCCAC	AGTGCCTCC	CTCCCTCTGC	CCTTCTCTGT	2340
CCACCCCTC	CTAAGCTAGA	CAAATCAACC	TTGTGCCTAA	TGGAGGAAGT	GTGGAAACTT	2400
TGTAAAATGT	GTACATAGGA	CTTGGAGACC	TTGTGTCCGC	CCTGCTCTTT	CTTCCGATCC	2460
CACAGGAAGT	GCCCCTGCAC	TGTCATCACT	CTCACGAGGA	CGTCACCTGT	GCTAACCTGG	2520
GGGAAGGTGG	GGTCCTTTCT	TCTTTCCTTT	TGAGAAGCAC	TGAAACTCCC	AAGTGTGTTC	2580
TTATCCCATG	GATAGGAAAC	CAGTGAATTC	CGTGGCTGGC	ACACCACGAG	CTGTCAATGC	2640
GCACGGGTCA	TAACACATCT	GGGTGTCATC	GGACACCTCA	CCTCGCCAC	CCTGTAGGAG	2700
CGTAAGGAGC	CTCCATCCTC	AGCCACGTGC	AGCTGACGTG	GCTTTCCTGA	TCGGAGGGCT	2760
TTTCTTTTAT	GGGTGGCCCA	GCTTCTTCAA	GACCTTCACT	GCTCTGCCTC	AGTGGACAGT	2820
CGTTTCTTTT	TTGAGGTGTG	ACCTTTTGTT	TTCATGCCTT	CCCCTGAAG	TCATCCTGTG	2880
TTTTGTAAATC	AGCTGTCAGG	CCAAATGTCT	GACCCGAAAG	AGAATGTATT	TAACTCATG	2940
CTGCGTTGTT	CAGCAGCCCC	TCTGTGTTCT	GTGTGATTTG	TTTTATTTTT	CCTTTTTTTT	3000
ACATATATAT	GCAGGGAAGT	AATGGTACTG	GATAGTGTATG	TTTTCTATGT	GGTTCAAATA	3060
TGAATTTTCGA	ACACACCAAG	CCGCTAATGA	GATAGCAGCT	TTTTTCTGGG	ACCCAGAGTC	3120
ACAACCAAAT	TGATTTAAGA	CCGGACCCAA	GACACCTTTA	ACAATAGGAC	TGAAAGGAAA	3180
AAGGATAGGG	AAAAAGCTTA	TTAAAGAAAT	GTGTCAACAC	CAAATGTAGA	GGGGAAGAAC	3240

CACAACCAGG CATAATACCA AACCGGTTCC AGGGGGAAAC AAGGCTTTGG TATTCCGCTG	3300
GCTCCAGCGC TTTTCTGAA ACCCGAGGCT GGCCAGGGTG CTGTCACCGT GTGGTCTTTG	3360
ATTGCAGCCA TTCAATGCCC ACATGCTTTT CCTTCTTGTT TCAGAACAGC ACATGGTCAC	3420
AACAAGATAT TTTCTTTCCC TCCAAAGCCT TTTGTCTCCT TGTGCCTCTT TTTATCCTTA	3480
GGAAAAGATC CAGGTGCTTG TGAAAAGAAT CATGAATGCA ACAAGGGAGG CTGGTCTCTG	3540
TGCTGTGCGC GATTAAGTTT TAAACTTTTA TTTATTATTT ATGTCTGCCG TATTTTAAAT	3600
AAACATTCTC GTTCCTTCCA GTTCCAGTCA TAGTGTGTCT GTGGCATTCC AGTCCAACCA	3660
TGTGACTTAT TTATTCTAAT TTGAGGGCTG CACTGTACAC CATGGTGTCC TGTGACACCG	3720
TGTTCCAGAC ATTTATGGAA GGAAAACATC CCATATAAAT GAAACTGTCA TGCTGTGTCC	3780
TCCCCGGCAG CAGAAGATGT GTCCTTCCAT TGAGTGAGGG TAACCTTATG TCCACCAAGG	3840
ATACTTTGAG AAAGCCCCTA AGGAACAAGC CTCAGTCCCA CGGTTTCAGA CTATTTATTC	3900
TCTGAACACA AGAGTATTGG TTAATTATGT TCTCAGCTCT CCCTGCTGTT GTATGTGTGC	3960
ATTCACTGCA AGTAACTTAT ATCTTTTTAT TTGAATGTAT TT'TAAAGCAG TAGATAGAAT	4020
AACAAAGGAA TATGAAAACC ATGGACTGAA TGGACCATTT TATGTATTCA GAGAGAGAAG	4080
CCACTCATCA TTGCCAGAAA TACCATGTAA AAATTGGCAG TTCAGAGGTT GCAATACTTA	4140
GTATAGTAAA TAAATAAACG GTCAACATTG TGCAACCACT ACCAAAAAGT GTGTTGTAAT	4200
GCATCAAAAA TCAACACAAT TTTATTCACT AATGAGTATC AATAAAATAA GTTCAAATGA	4260
TGGAAACCAC AAAAAAAAAA AAAAA	4285

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met	Gln	Arg	Asn	Val	Lys	Gln	Gln	Lys	Lys	Thr	Ala	Gly	Ser	Asp	Leu
1				5				10						15	
Arg	Arg	Glu	Thr	Lys	Phe	Ile	Pro	Gln	Arg	Pro	Ile	Asn	Pro	Thr	Pro
			20					25					30		
Leu	Ala	Ser	His	Pro	Gln	Thr	Gly	Ser	Thr	Thr	Gly	Pro	Arg	Ile	Leu

35					40					45					
Met	Arg	Asn	Leu	Val	Trp	Ile	Gly	Ser	Glu	Ala	Gly	Ile	Trp	Cys	Ser
50						55					60				
Ala	Asp	Gln	Cys	Ser	Lys	Leu	Trp	Leu	Phe	Leu	Arg	Thr	Arg	Leu	Gln
65					70					75				80	
Ser	Arg	Thr	Phe	Ala	Phe	His	Leu	Pro	Arg	Pro	Asp	Pro	Val	Asn	Lys
				85					90					95	
Val	Ala	His	His	Phe	Leu	His	Leu	Leu	Ser	Asp	Met	Leu	Asp	Phe	Asn
			100					105					110		
Phe	Tyr	Cys	Gly	Cys	Thr	Trp	Met	Gln	Gly	Ile	Cys	Phe	Val	Pro	Pro
	115						120					125			
Asn	Leu	Ala	His	His	Pro	Gly	Lys	Cys	Met	Ser	Gln	Thr	Asn	Ser	Thr
130						135					140				
Phe	Thr	Phe	Thr	Thr	Cys	Arg	Ile	Leu	His	Pro	Ser	Asp	Glu	Leu	Thr
145					150					155				160	
Arg	Val	Thr	Pro	Ser	Leu	Asn	Ser	Ala	Pro	Thr	Pro	Ala	Cys	Gly	Ser
				165					170					175	
Thr	Ser	His	Leu	Lys	Ser	Thr	Pro	Val	Ala	Thr	Pro	Cys	Thr	Pro	Arg
			180					185					190		
Arg	Leu	Ser	Leu	Ala	Glu	Ser	Phe	Thr	Asn	Thr	Arg	Glu	Ser	Thr	Thr
	195						200					205			
Thr	Met	Ser	Thr	Ser	Leu	Gly	Leu	Val	Trp	Leu	Leu	Lys	Glu	Arg	Gly
210						215					220				
Ile	Ser	Ala	Ala	Val	Tyr	Asp	Pro	Gln	Ser	Trp	Asp	Arg	Ala	Gly	Arg
225					230					235				240	
Gly	Ser	Leu	Leu	His	Ser	Tyr	Thr	Pro	Lys	Met	Ala	Val	Ile	Pro	Ser
				245					250					255	
Thr	Pro	Pro	Asn	Ser	Pro	Met	Gln	Thr	Pro	Thr	Ser	Ser	Pro	Pro	Ser
			260				265						270		
Phe	Glu	Phe	Lys	Cys	Thr	Ser	Pro	Pro	Tyr	Asp	Asn	Phe	Leu	Ala	Ser
	275						280					285			
Lys	Pro	Ala	Ser	Ser	Ile	Leu	Arg	Glu	Val	Arg	Glu	Lys	Asn	Val	Arg
290						295					300				
Ser	Ser	Glu	Ser	Gln	Thr	Asp	Val	Ser	Val	Ser	Asn	Leu	Asn	Leu	Val
305					310					315				320	
Asp	Lys	Val	Arg	Arg	Phe	Gly	Val	Ala	Lys	Val	Val	Asn	Ser	Gly	Arg
				325					330					335	
Ala	His	Val	Pro	Thr	Leu	Thr	Glu	Glu	Gln	Gly	Pro	Leu	Leu	Cys	Gly

340	345	350
Pro Pro Gly Pro Ala Pro Ala Leu Val Pro Arg Gly Leu Val Pro Glu		
355	360	365
Gly Leu Pro Leu Arg Cys Pro Thr Val Thr Ser Ala Ile Gly Gly Leu		
370	375	380
Gln Leu Asn Ser Gly Ile Arg Arg Asn Arg Ser Phe Pro Thr Met Val		
385	390	395
Gly Ser Ser Met Gln Met Lys Ala Pro Val Thr Leu Thr Ser Gly Ile		
405	410	415
Leu Met Gly Ala Lys Leu Ser Lys Gln Thr Ser Leu Arg		
420	425	

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

ACTTTGAATT TTTTATTTGT GAAATTAAAA ATATGGTATT ATATATATAT AAACCTTCTAT	60
TCCTCTATAA ATATAGATGA TTTTGTGATA GTGAACAGAA TAAATGTATA CCAAATTCAA	120
AGACCAATAT CATTTTAGCG TATGACAGAC ATAGATAAAT TTAGGTCCTA AGTACCGGCA	180
TTTTGATAAA TTCTTAAAGT TTAACAACAT ACAATCAGGA GGATTGCTTT TCTCCTCTTC	240
TTCACAGAGA ACTAAAGTGA ATATTTTAA ATGGCTTTGA AAGATTTACA TTTGACACAT	300
TTCTGTAAAT CCAAAGAGG AGCACACAGG GATTTAATGC AGTAGACCTG CACACATTTT	360
CCCTTTAGCA TGCATGCCCA TATTTTGTTC ATTTTCAGGCG CTATCTCCCC GTCAATTATT	420
CCACCTTCTT TACCTCCTGA AATCTTACCA GGTTATTATT GGTGGTGTGA ATTGTTCCCC	480
CCTCAGAATG TGCTGCTGAA TAATAATCGT AATAAAATGT TGAAAGTGTA CAACTTTTAC	540
ATTTTAAAGT TTCTGATATA TGTCTAGTTA TTTGATTAAA AATAAGAAAA TAGCACTTCA	600
TTTTGAGGAA GTCCATGACA CTGAAATATC CTTCAAGTTT TCAATTTCTG TTTACGTTTT	660
GCTGTCTTGT TAAGGAAAGC AAACATCAAC TCCTTAACAA AGCTTTCCAG GTGACCTCAA	720
CATTTCCATT TTACAGACCG GTAAAATCTA AGCGCAGGCT GTCTCATTCT CAAAGGCAAG	780
GTTGCCAGGC ATCCGTATGC AATTAGAATT AACATTTTAT AACCCATATC TTCAGTCTCT	840

TCCAACCCAC	ACAAAGCTTC	ATGCTTCTTC	CCAAATCTCA	GTAACCACAT	CTTTCCATGA	900
CGCTGGCCAA	ACCCATACCA	GGTTTTAGAC	ACTAGAGAAT	GAAATGAGCT	CACCCCTCAA	960
AAATTAGACT	TCAAAAAGTT	TGGCATTGGT	TATCTCACTC	ACCCTGTAAC	CAACTAAGGT	1020
GGGAGAAGGG	AGTGTCTGGC	GTTGAAGGTG	ACCGTGGAGG	GAGGCTGAGA	CTGCCAGCGC	1080
CCACACCCGT	GGGCCCCCAT	GAAGTTGGAG	GAAAGTTCTG	GACAGTTAAA	AATCCAGCTT	1140
CAGGAAGTCG	AAGGGACGGG	CCTTCGCAAT	CCACCGCCGA	GCAAGGGAGG	AATTGTAATG	1200
TATGGGGGCC	CTCCTCCAGA	TTTGGAAGGT	TTGTGGAGTT	CTGTACCTTA	AGAGCCCCTA	1260
CCTCAAGCCA	GGAAAGAAAG	GGAGGGGACA	GAAGGAGGGG	GAGGGGGCAA	AAGGAGGAGG	1320
CGGGAAGTGA	CCCTGGCAGC	GCAGCCCTAG	TCGCACCCCG	CAGTGCTGAA	CTCGCCCCGG	1380
AGCTGGCGCC	CAGCCGTCCC	GAGCACCCGT	GGTAGGGAGA	GGCGCGCGAG	GACGACCAGG	1440
AGCGCTGTGC	GGTTGCACAC	CAGTTTTAGC	TCCTTTGCAA	TACTCCGAAA	AGGGCAAGAA	1500
GAAAAGCCTC	AAATGGTTAA	ACCGCCCTAA	ATAATTAAAA	ACTTTTGAAA	AAGAAAAACG	1560
CGTGATCGGT	CGTCATTTAA	ATACAAATAT	ACTTACAAAA	ATCCTACACA	GGCTATTTAC	1620
AATCATAAAA	GCGAACAGTC	CTGGTACCAG	AGTGTGAGGG	CAAGAGGTCT	GTCCATCCTC	1680
CCTCTGGCAG	TCGGGCCCTC	GTGTCCTTTT	GCCTCAGGGA	CGGAAGCTTT	TGCAGGAGCT	1740
GAGTTGTTCT	AGGCCTCTTT	GGCCGAATTC	GGCCAAAGAG	GCCTAATTCC	TTCCTCGGTT	1800
ATTTCAATTCA	GAGAATATTT	ATGAAATGCC	TACTGTGTGC	AAGTCATCCA	TCCTTGAAAA	1860
GGCCACTTCT	CAGTGAGGGA	GAGATGTAGT	GGATTCTGTG	AGACATACCT	GCTGGAGTTG	1920
AAGCAGTAAA	TAGCATGTCT	TCCCCCTCCC	CGATCTTAAG	GTGTGTTTTT	TAGAAAAGTT	1980
CCCTAATGGA	ATTCATGAGT	TTGGGGGTCT	CAGTCACCCG	CTTGCCTGTA	GGATTCCATT	2040
TGATGATTCT	GGATTTTTGC	TGTTTGTTAT	TGCCCTTAGA	GGGGCTCTGA	GTATCTACTT	2100
GTGGGTGGCC	ATTTCTTGAC	ATCTGCATGT	ACCTCGTGGA	ATTCAGCCAG	CTTCATGTTG	2160
CAAATCAGAA	AGCTGACCCC	AAGACTGCAA	ATCAATGAAG	GTATTGGCAT	TGTTAAGGTC	2220
GTAGCGTAGA	CAACAGCAGT	CATAAATAAT	TAGGCAGGAA	CTTAACCCAA	ATCTAGTTCT	2280
TTGACCACCT	CTACCACCAG	AACCCAGCAG	AACTCACAT	CTCCTGATAA	GAGTTGCTGG	2340
ACTCGATGTT	TTTGTTTTGC	ATTTTCTCCT	CTCCTTCCCC	ACTTACTCAG	AGAATTTAAA	2400
GTCTGTAGAG	TCAGCACAGC	CCCATCAGTC	CAGGAACTTC	CCACCACCAG	CCCTTGACTG	2460
TCCCATTAAC	TGACATGGTC	AGATTTCCAG	CTCCCCCTAC	TCCCTGCTGT	GAAACAATCC	2520

CTCTCCYTGT GAGAGGAAAY TGC GCGSGAA GGYTAAGGGA GTGTGGCGGG CGGYTCCGGG	2580
AGCCAACATG CCTCGGTATG CGCAGCTGKT CATGGSCCCC GCGGGCAGCG GGAAGAGCAC	2640
YTACTGTGCC ACCATGGTCC AGCACTGTGA AGCCYTCAAC CGGTCTGTCC AAGTTGTAAA	2700
CCTGGATCCA GCAGCAGAAC ACTTCAAYTA CTCCGTGATG GCTGACATCC GGGAACTGAT	2760
CGAGGTGGAT GATGTAATGG AGGATGATTY TYTGCGATTG GGTCCCAACG GAGGATTGGT	2820
ATTTTGCATG GAGTACTTTG CCAATAATTT TGACTGGCTG GAGAACTGTC TTGGCCATGT	2880
AGAGGACGAC TATATCCTTT TTGATTGTCC AGGTCAGATT GAGTTGTACA CTCACCTGCC	2940
TGTGATGAAA CAGCTGGTCC AGCAGCTCGA GCAGTGGGAG TTCCGAGTCT GTGGAKTTTY	3000
TYTTGTTGAT TCTCAGTTCA TGGTGGAGTC ATTCAAGTTT ATTTCTGGCA TCTTGGCAGC	3060
CCTGAGTGCC ATGATCTCTC TAGAAATTCC GCAAGTCAAC ATCATGACAA AAATGGATCT	3120
GCTGAGTAAA AAAGCAAAAA AGGAAATTGA GAAATTTTTA GATCCAGACA TGTATTCTTT	3180
ATTAGAAGAT TCTACAAGTG ACTTAAGAAG CAAAAAATTC AAGAACTGA CTAAAGCTAT	3240
ATGTGGACTG ATTGATGACT ACAGCATGGT TCGATTTTTA CCTTACGATC AGTCAGATGA	3300
AGAAAGCATG AACATTGTAT TGCAGCATAT TGATTTTGCC ATTCAATATG GAGAAGACCT	3360
AGAATTTAAA GAACCAAAGG AACGTGAAGA TGAGTCTTCC TCTATGTTTG ACGAATATTT	3420
TCAAGAATGC CAGGATGAAT GAAGAGTTTA CTAAAAGTAA CCATCTAAAG AGCTTGTGGC	3480
CAAACCAGCA GAACATTCTT CTYTTCAAAG GATGCAATAG TAGAAAGCTA CTTATTTTAA	3540
TGAAAAAAG TAAAACTTCG TTCTTTATCA GCCTCATGCC TGAATCAAAT TTTTAATTAT	3600
TCTGAAACTG CTGCTGTTTA AAGTGGAAATC TTTTAGTATT ATAACAGCAT CACTTTAGAT	3660
TTTGTAAGTC AAAATTGAAA TGAATGCACA TAGATTTATA TATAAATTAG CACCTGAGCT	3720
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	3751

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Pro Arg Tyr Ala Gln Leu Xaa Met Xaa Pro Ala Gly Ser Gly Lys

1	5	10	15
Ser Thr Tyr Cys Ala Thr Met Val Gln His Cys Glu Ala Xaa Asn Arg	20	25	30
Ser Val Gln Val Val Asn Leu Asp Pro Ala Ala Glu His Phe Asn Tyr	35	40	45
Ser Val Met Ala Asp Ile Arg Glu Leu Ile Glu Val Asp Asp Val Met	50	55	60
Glu Asp Asp Xaa Leu Arg Phe Gly Pro Asn Gly Gly Leu Val Phe Cys	65	70	75
Met Glu Tyr Phe Ala Asn Asn Phe Asp Trp Leu Glu Asn Cys Leu Gly	85	90	95
His Val Glu Asp Asp Tyr Ile Leu Phe Asp Cys Pro Gly Gln Ile Glu	100	105	110
Leu Tyr Thr His Leu Pro Val Met Lys Gln Leu Val Gln Gln Leu Glu	115	120	125
Gln Trp Glu Phe Arg Val Cys Gly Xaa Xaa Xaa Val Asp Ser Gln Phe	130	135	140
Met Val Glu Ser Phe Lys Phe Ile Ser Gly Ile Leu Ala Ala Leu Ser	145	150	155
Ala Met Ile Ser Leu Glu Ile Pro Gln Val Asn Ile Met Thr Lys Met	165	170	175
Asp Leu Leu Ser Lys Lys Ala Lys Lys Glu Ile Glu Lys Phe Leu Asp	180	185	190
Pro Asp Met Tyr Ser Leu Leu Glu Asp Ser Thr Ser Asp Leu Arg Ser	195	200	205
Lys Lys Phe Lys Lys Leu Thr Lys Ala Ile Cys Gly Leu Ile Asp Asp	210	215	220
Tyr Ser Met Val Arg Phe Leu Pro Tyr Asp Gln Ser Asp Glu Glu Ser	225	230	235
Met Asn Ile Val Leu Gln His Ile Asp Phe Ala Ile Gln Tyr Gly Glu	245	250	255
Asp Leu Glu Phe Lys Glu Pro Lys Glu Arg Glu Asp Glu Ser Ser Ser	260	265	270
Met Phe Asp Glu Tyr Phe Gln Glu Cys Gln Asp Glu	275	280	

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TNCAGGCCTT GCGTTCCTAG CTGCTCTGC

29

- (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GNGCTGTGAG TTTATCCACA AAGGAACAG

29

- (2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GNATAGGAGG TCCCAAGTTA TCAAGGTTT

29

- (2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:
GNTTTCCTGG TTCTTGGTCA GGTTTCCTC 29

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
CNAGATGCAA TGGTTGTGAG ATTGACCAA 29

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
GNCACTTTCC ACTGCTGTGA GCTTGTCAT 29

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
ANCAGACAGT TTGCCATGGA GTACATCAC 29

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TNATGAACCA CAGGAAACAG GAAGCCGTC

29

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TNAAGGTGAA GGTGGAGTTG GTCTGAGAC

29

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GNCAGAAATA AACTTGAATG ACTCCACCA

29

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Asn Ser Gln Leu Asn Ser Phe Thr Gly Gln Met Glu Asn Ile Thr
1 5 10 15
Thr Ile Ser Gln Ala Asn Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu
20 25 30
His Lys Asp Ala Glu Asn Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu
35 40 45
Glu Arg Phe Gln Leu Phe Glu Thr Asp Ile Val Asn Ile Ile Ser Asn
50 55 60
Ile Ser Tyr Thr Ala His His Leu Arg Thr Leu Thr Ser Asn Leu Asn
65 70 75 80
Glu Val Arg Thr Thr Cys Thr Asp Thr Leu Thr Lys His Thr Asp Asp
85 90 95
Leu Thr Ser Leu Asn Asn Thr Leu Ala Asn Ile Arg Leu Asp Ser Val
100 105 110
Ser Leu Arg Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu
115 120 125
Val Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser
130 135 140
Lys His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro
145 150 155 160
Gly Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly
165 170 175
Pro Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro
180 185 190
Pro Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro
195 200 205
Gly Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly
210 215 220
Ser Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp
225 230 235 240
Pro Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln
245 250 255
Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly
260 265 270

Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met
 275 280 285
 Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val
 290 295 300
 Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn
 305 310 315 320
 Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe
 325 330 335
 Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp
 340 345 350
 Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp
 355 360 365
 Ile Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr
 370 375 380
 Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro
 385 390 395 400
 Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly
 405 410 415
 His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp
 420 425 430
 Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp
 435 440 445
 Arg Glu Thr Val Leu Ser Ser Ala Leu
 450 455

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Cys Gly His His Glu Leu Asn Asn Leu Asn Leu Thr Gln Val Gln Gln
 1 5 10 15
 Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val Asp Asp Thr Ser Gln
 20 25 30

Ala	Ile	Gln	Arg	Ile	Lys	Asn	Asp	Phe	Gln	Asn	Leu	Gln	Gln	Val	Phe	35	40	45	
Leu	Gln	Ala	Lys	Lys	Asp	Thr	Asp	Trp	Leu	Lys	Glu	Lys	Val	Gln	Ser	50	55	60	
Leu	Gln	Thr	Leu	Ala	Ala	Asn	Asn	Ser	Ala	Leu	Ala	Lys	Ala	Asn	Asn	65	70	75	80
Asp	Thr	Leu	Glu	Asp	Met	Asn	Ser	Gln	Leu	Asn	Ser	Phe	Thr	Gly	Gln	85	90	95	
Met	Glu	Asn	Ile	Thr	Thr	Ile	Ser	Gln	Ala	Asn	Glu	Gln	Asn	Leu	Lys	100	105	110	
Asp	Leu	Gln	Asp	Leu	His	Lys	Asp	Ala	Glu	Asn	Arg	Thr	Ala	Ile	Lys	115	120	125	
Phe	Asn	Gln	Leu	Glu	Glu	Arg	Phe	Gln	Leu	Phe	Glu	Thr	Asp	Ile	Val	130	135	140	
Asn	Ile	Ile	Ser	Asn	Ile	Ser	Tyr	Thr	Ala	His	His	Leu	Arg	Thr	Leu	145	150	155	160
Thr	Ser	Asn	Leu	Asn	Glu	Val	Arg	Thr	Thr	Cys	Thr	Asp	Thr	Leu	Thr	165	170	175	
Lys	His	Thr	Asp	Asp	Leu	Thr	Ser	Leu	Asn	Asn	Thr	Leu	Ala	Asn	Ile	180	185	190	
Arg	Leu	Asp	Ser	Val	Ser	Leu	Arg	Met	Gln	Gln	Asp	Leu	Met	Arg	Ser	195	200	205	
Arg	Leu	Asp	Thr	Glu	Val	Ala	Asn	Leu	Ser	Val	Ile	Met	Glu	Glu	Met	210	215	220	
Lys	Leu	Val	Asp	Ser	Lys	His	Gly	Gln	Leu	Ile	Lys	Asn	Phe	Thr	Ile	225	230	235	240
Leu	Gln	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Pro	Arg	Gly	Asp	Arg	Gly	Ser	245	250	255	
Gln	Gly	Pro	Pro	Gly	Pro	Thr	Gly	Asn	Lys	Gly	Gln	Lys	Gly	Glu	Lys	260	265	270	
Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Glu	Arg	Gly	Pro	Ile	Gly	275	280	285	
Pro	Ala	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Gly	Lys	Gly	Ser	Lys	Gly	Ser	290	295	300	
Gln	Gly	Pro	Lys	Gly	Ser	Arg	Gly	Ser	Pro	Gly	Lys	Pro	Gly	Pro	Gln	305	310	315	320
Gly	Pro	Ser	Gly	Asp	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Lys	Glu	Gly	325	330	335	

Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr
 340 345 350

Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro
 355 360 365

Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly
 370 375 380

Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro
 385 390 395 400

Ala Pro Glu Asp Asn Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp
 405 410 415

Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys
 420 425 430

Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg
 435 440 445

Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val Gly Arg Glu Ser His
 450 455 460

Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu
 465 470 475 480

Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp
 485 490 495

Asn Trp Gly His Gly His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile
 500 505 510

Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe
 515 520 525

Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser Ser Ala Leu
 530 535 540